

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 22, 2004, 11:49:33 ; Search time 36 Seconds
(without alignments)

2164.805 Million cell updates/sec

Title: US-10-620-049-23

Sequence: 1 DQMTQTSSLSASLGDRVT.....GLRYAMDYWGQGTSTVSS 247

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: sp archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	535	40.6	614	11	Q7MT6 mus musculus
2	524.5	39.8	234	11	Q91WP8 mus musculus
3	486	36.9	111	11	Q9DPB8 mus musculus
4	483.5	36.7	110	11	Q9UL83 mus musculus
5	480.5	36.5	233	11	Q91WS9 mus musculus
6	478	36.3	474	11	Q8R3H6 mus musculus
7	471	35.8	142	11	Q924Q1 mus musculus
8	470	35.7	481	11	Q91WT1 mus musculus
9	469.5	35.6	145	11	Q924Q6 mus musculus
10	465.5	35.3	145	11	Q924Q9 mus musculus
11	464.5	35.3	145	11	Q924R1 mus musculus
12	464.5	35.3	145	11	Q924R4 mus musculus
13	463.5	35.1	118	11	Q921C4 mus musculus
14	462.5	35.0	234	11	Q924Q3 mus musculus
15	461	35.0	146	11	Q924Q3 mus musculus
16	459.5	34.9	482	11	Q8K172 mus musculus

17	458.5	34.8	145	11	Q924P7 mus musculus
18	458	34.8	473	11	Q924P4 mus musculus
19	456.5	34.7	143	11	Q924R0 mus musculus
20	455.5	34.6	488	11	Q8K0F2 mus musculus
21	454	34.5	140	11	Q924R2 mus musculus
22	452	34.3	146	11	Q924R8 mus musculus
23	450.5	34.2	613	11	Q8VCX7 mus musculus
24	449.5	34.1	143	11	Q924Q0 mus musculus
25	446	33.9	117	11	Q90XB9 mus musculus
26	445	33.9	480	11	Q8K0Z4 mus musculus
27	445.5	33.8	473	11	Q91J25 mus musculus
28	444	33.7	168	11	Q9VDC9 mus musculus
29	440.5	33.4	143	11	Q924P9 mus musculus
30	440	33.4	140	11	Q924P8 mus musculus
31	439.5	33.4	137	11	Q924R6 mus musculus
32	439	33.3	146	11	Q924Q8 mus musculus
33	436.5	33.1	141	11	Q924Q4 mus musculus
34	436.5	33.1	463	11	Q91JC4 mus musculus
35	436	33.1	142	11	Q924Q2 mus musculus
36	435.5	33.1	145	11	Q924Q7 mus musculus
37	435	33.0	144	11	Q924P5 mus musculus
38	433.5	32.9	136	11	Q7PE3 mus musculus
39	433	32.9	470	11	Q7TK1 mus musculus
40	432.5	32.8	110	11	Q91J77 mus musculus
41	431.5	32.8	143	11	Q924P6 mus musculus
42	430.5	32.7	145	11	Q924R3 mus musculus
43	429.5	32.6	143	11	Q924Q5 mus musculus
44	428.5	32.5	143	11	Q924R7 mus musculus
45	428.5	32.5	243	11	Q7QW2 mus musculus

ALIGNMENTS

RESULT 1
ID Q7MT6 PRELIMINARY; PRT; 614 AA.
AC Q7MT6:
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6NCR; TISSUE=Hematopoietic Stem Cell;
RX MEDLINE=22388257; PubMed=12477937;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Schaefer C.F., Shat N.K., Alekshun S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan B., Moore T., Wax S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Umed T.B., Toshitsuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mulvaney S.J., Boeck S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Wortley K.C., Hale S., Garcia A.M., Gay L.U., Hulyk S.W., Villalón D.K., Wuzny D.W., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A., Walting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S., Krzywicki M.I., Skalska U., Small D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
SEQUENCE FROM N.A.
RC STRAIN=C57BL/6NCR; TISSUE=Hematopoietic Stem Cell;

RA Strausberg R.;
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC053409; AAH53409.1; -
 KW Hypothetical protein.
 SQ SEQUENCE 614 AA; 67746 MW; 839BAF3B8D124F89 CRC64;

Query Match 40.6%; Score 535; DB 11; Length 614;
 Best Local Similarity 82.9%; Pred. No. 8.3e-37;
 Matches 102; Conservative 7; Mismatches 14; Indels 0; Gaps 0;

QY 125 GGGGSGVQLQSGPELVKPGASVKISCKDGYANSSGMWVYKORPGQGLEWIGRIYPDG 184
 DB 16 GVASQVQLQSGPELVKPGASVKISCKASGYAFSSMMWVKORPEKGLEWIGRIYPDG 75

QY 185 DSNYNGKFEKALITLADKSSSTAYVQSLTSVDSAVYFCARSGLRVANDYWGQSTVY 244
 DB 76 DTVYNGKFKKXKATLTLDKSSSTAYVQSLTSVDSAVYFCARDYGSYFAVWQGTLT 135

QY 245 VSS 247
 DB 136 VSA 138

RESULT 2

Q91WF8 PRELIMINARY; PRT; 234 AA.

AC Q91WF8; 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Colon;
 RA Strausberg R.;
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC015292; AAH15292.1; -
 DR GO: GO:0005622; C:intracellular; IEA.
 DR GO: GO:0005840; C:ribosome; IEA.
 DR GO: GO:0003735; F:structural constituent of ribosome; IEA.
 DR GO: GO:0006412; F:protein biosynthesis; IEA.
 DR InterPro: IPR007110; IG-like.
 DR InterPro: IPR003006; IG_MHC.
 DR InterPro: IPR003596; IG_V.
 DR InterPro: IPR001865; Ribosomal_S2.
 DR Pfam: PF00047; IG; 2.
 DR SMART: SM00406; IGV; 1.
 DR PROSITE: PS00835; IG_LIKE; 2.
 DR PROSITE: PS00290; IG_MHC; 1.
 DR PROSITE: PS00862; RIBOSOMAL_S2_1; 1.
 KM Hypothetical protein.
 SQ SEQUENCE 234 AA; 25929 MW; B0D0B0E6EB7812D2 CRC64;

Query Match 39.8%; Score 524.5; DB 11; Length 234;
 Best Local Similarity 52.0%; Pred. No. 1.9e-36;
 Matches 116; Conservative 12; Mismatches 44; Indels 51; Gaps 4;

QY 1 DIQWTTSTSSASLGRVYSGASODIRYLNWYKORPDGYKPLIYTSLLQPGVPS 60
 DB 21 DIQWTTSTSSASLGRVYSGASODIRYLNWYKORPDGYKPLIYTSLLQPGVPS 80

QY 61 RFGSGSGGTDTSLTINNLEQEDIGYFCQOGNTPPMTFGGTGKLEIKSGGSGSDGSGG 120
 DB 81 RFGSGSGGTDTSLTINNLEQEDIGYFCQOGNTPPMTFGGTGKLEIKSGGSGSDGSGG 128

QY 121 GGGSGGSGEVQLQSGPELVKPGASVKISCKDGYANSSGMWVYKORPGQGLEWIGRIY 180
 DB 129 --ADAAAPVSIFFPSSSQLTSGASV-----VCFINNFY 160

QY 181 PG-----DGDNNYNGKFEKALITLADKSSSTAYVQSLTS 215
 DB 161 PKDINWVKKIDGSEKRGVGLNS---WTDQSGKSTGYSMSSTLT 200

RESULT 3

Q9D9B8 PRELIMINARY; PRT; 111 AA.

AC Q9D9B8; 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Adult male testis cDNA, RIKEN full-length enriched library,
 DE clone:170011011, full insert sequence.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Aikawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana K.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Glisic C., King B., Kochwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Mikaido I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Steubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Funuo M., Aono H., Batdarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carinci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima U., Mazzarelli U., Vombatus P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seta T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohetsuki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection."
 RL Nature 409:685-690(2001).
 DR EMBL: AK007163; BAB24877.1; -
 DR HSP: P01810; 2PBJ.
 DR InterPro: IPR007110; IG-like.
 DR InterPro: IPR003596; IG_V.
 DR Pfam: PF00047; IGV; 1.
 DR SMART: SM00406; IGV; 1.
 DR PROSITE: PS00835; IG_LIKE; 1.
 DR PROSITE: PS00862; RIBOSOMAL_S2_1; 1.
 SQ SEQUENCE 111 AA; 11976 MW; 874DFF7BD98BD7B2 CRC64;

Query Match 36.9%; Score 486; DB 11; Length 111;
 Best Local Similarity 90.2%; Pred. No. 1.3e-33;
 Matches 92; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 125 GGGGSGVQLQSGPELVKPGASVKISCKDGYANSSGMWVYKORPGQGLEWIGRIYPDG 184
 DB 3 GVASQVQLQSGPELVKPGASVKISCKASGYAFSSMMWVKORPEKGLEWIGRIYPDG 62

QY 185 DSNYNGKFEKALITLADKSSSTAYVQSLTSVDSAVYFCAR 226
 DB 63 DTVYNGKFKKXKATLTLDKSSSTAYVQSLTSVDSAVYFCAR 104

RESULT 4

Q9JL83 PRELIMINARY; PRT; 110 AA.

AC Q9JL83; 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Anti-myosin immunoglobulin heavy chain variable region
 DE (fragment).

OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BAJB/c;
 RX MEDLINE=20448942; PubMed=10922488;
 RA Maltiel S, Liao L, Cunningham M.W., Diamond B;
 RT "T-cell-dependent antibody response to the dominant epitope of
 streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive
 with cardiac myosin.";
 RT Infect. Immun. 68:5803-5808 (2000).
 DR EMBL; AF060623; AAF69321.1; -.
 DR HSSP; P01810; 2FBJ.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig_1.
 DR SMART; SM00406; IGv_1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 DR NON_TER 1
 FT NON_TER 110
 SQ SEQUENCE 110 AA; 12052 MW; 84E6F2AD219AF95E CRC64;

Query Match 36.7%; Score 483.5; DB 11; Length 110;
 Best Local Similarity 83.9%; Pred. No. 2,1e-33;
 Matches 94; Conservative 7; Mismatches 8; Indels 3; Gaps 2;

QY 137 PELVPGASVKTSCDSGYAFNSMMNWKORPGGLEMIGRYGDDSNYNGFEKKA 196
 DB 1 PELVPGASVKTSCDSGYAFNSMMNWKORPGGLEMIGRYGDDSNYNGFEKKA 60
 QY 197 ITTADKSSSTAYMOLSLTSVDSAVYFCARSGL-IRYANDYWGQSTVTS 247
 DB 61 TTTADKSSSTAYMOLSLTSVDSAVYFCARSGL-IRYANDYWGQSTVTS 110

RESULT 5
 Q91WS9 PRELIMINARY; PRT; 233 AA.
 ID Q91WS9;
 AC Q91WS9;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Colon;
 RA Strauberg R.;
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC013496; AAH13496.1; -.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PR00047; Ig_2.
 DR SMART; SM00406; IGv_1.
 DR PROSITE; PS50835; IG_LIKE; 2.
 DR PROSITE; PS00290; IG_MHC; 1.
 KM Hypothetical protein.
 FT NON_TER 1
 SQ SEQUENCE 233 AA; 25781 MW; B1C184DA149A16EB CRC64;

Query Match 36.5%; Score 480.5; DB 11; Length 233;
 Best Local Similarity 48.9%; Pred. No. 9,8e-33;
 Matches 109; Conservative 11; Mismatches 52; Indels 51; Gaps 4;
 QY 1 D1QMPOTTSLSASLDRTVVCRAQDRIYNYLWYQKPGDGVFLIYTSRLQPGVPS 60
 DB 20 D1QMPOTTSLSASLDRTVVCRAQDRIYNYLWYQKPGDGVFLIYTSRLQPGVPS 79

QY 61 RFGSGSGDYSLTINLEQEDIGYFCQGNTPPTFGGKLEIKRGGGSGDGGSGSG 120
 DB 80 RFGSGSGDYSLTINLEQEDIGYFCQGNTPPTFGGKLEIKRGGGSGDGGSGSG 127
 QY 121 GGSGGGGSEVQLQSGPELVKPGASVKSCKDSGYAFNSMMNWKORPGGLEMIGRY 180
 DB 128 --ADAAPVSIPEPSSSEQLTSGASV-----VCELANFY 159
 QY 181 PG-----DDSNYNGKEGKAILTADKSSSTAYMOLSLT 215
 DB 160 PVDINVKMIDKSGRONGVLS--WTDDSDSTYSMSSTILT 199

RESULT 6
 Q9R3H6 PRELIMINARY; PRT; 474 AA.
 ID Q9R3H6;
 AC Q9R3H6;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein.
 GN AU044919.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Strauberg R.;
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC025447; AAH25447.1; -.
 DR MGD; MGI:2144967; AU044919.
 DR GO; GO:0005489; F:Electron transporter activity; IEA.
 DR GO; GO:0006118; P:Electron transport; IEA.
 DR InterPro; IPR000345; Cytochrome_B5.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig_3.
 DR SMART; SM00406; IGv_1.
 DR PROSITE; PS00190; CYTOCHROME_C; 1.
 DR PROSITE; PS50835; IG_LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; 1.
 KM Hypothetical protein.
 SQ SEQUENCE 474 AA; 51748 MW; 8608B57C6CD2874A CRC64;

Query Match 36.3%; Score 478; DB 11; Length 474;
 Best Local Similarity 74.0%; Pred. No. 3,9e-32;
 Matches 91; Conservative 14; Mismatches 18; Indels 0; Gaps 0;

QY 125 GGSSEVQLQSGPELVKPGASVKSCKDSGYAFNSMMNWKORPGGLEMIGRY 184
 DB 16 GVHSQVQLQSGPELVKPGASVKSCKDSGYAFNSMMNWKORPGGLEMIGRY 75
 QY 185 DSNYNGKEGKAILTADKSSSTAYMOLSLTSVDSAVYFCARSGLLRYANDYWGQSTV 244
 DB 76 DTHYSGKFGKAKLTADKSSSTAYMOLSLTSVDSAVYFCARSDYGDYFDWGQATVT 135
 QY 245 VSS 247
 DB 136 VSS 138

RESULT 7
 Q924Q1 PRELIMINARY; PRT; 142 AA.
 ID Q924Q1;
 AC Q924Q1;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE V23-D-J-C mu protein (Fragment).
 GN V23-D-J-C MU

OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6;
 RA Kozono Y., Kozono H., Azuma T.,
 RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
 RT Affinity Maturation of B Cell Antigen Receptors in Response to (4-
 RT Hydroxy-3-Nitrophenyl)Acetyl (NP)."
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB069913; BAB63929.1; -
 DR PIR; F33932; F33932.
 DR PIR; F28833; F28833.
 DR PIR; PH1156; PH1156.
 DR PIR; PH1158; PH1158.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig_1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PSS0835; IG_LIKE; 1.
 FT NON_TER
 FT NON_TER
 SQ SEQUENCE 142 AA; 15622 MW; 24A265CE4EA4318B CRC64;

Query Match 35.8%; Score 471; DB 11; Length 142;
 Best Local Similarity 77.3%; Pred. No. 3.3e-32;
 Matches 92; Conservative 7; Mismatches 18; Indels 2; Gaps 1;
 Oy 129 EVQLQDSGPELVKPGASVKISCKDQGYAFNNSMMNWVKQRPQGGLRWIGRIYDGDSDNY 188
 Db 1 QVQLQQPGELVYKPGASVKISCKASGYTFSTYMMHWKQRPQGGLRWIGRIYDGDSDNY 60
 Oy 189 NGKFEKAITLADKSSSTAVYQLSLTSVDSAVYFCARSGILRYANDYMGQGSTVTVSS 247
 Db 61 NEKFKSKITLTVDSSTAVYQLSLTSVDSAVYFCARSGILRYANDYMGQGSTVTVSS 117

RESULT 8
 ID Q91WT1 PRELIMINARY; PRT; 481 AA.
 AC Q91WT1;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Hypothetical protein.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Colon;
 RA Strabberg R.;
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC013490; AAH13490.1; -
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig_1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PSS0835; IG_LIKE; 4.
 DR PROSITE; PSS00290; IG_MHC; 2.
 KW Hypothetical protein.
 SQ SEQUENCE 481 AA; 52105 MW; 97DF68DD159463F65 CRC64;

Query Match 35.7%; Score 470; DB 11; Length 481;
 Best Local Similarity 73.0%; Pred. No. 1.9e-31;
 Matches 92; Conservative 11; Mismatches 21; Indels 2; Gaps 1;
 Oy 122 GSGGGSGEVQLQDSGPELVKPGASVKISCKDQGYAFNNSMMNWVKQRPQGGLRWIGRIY 181
 Db 1 QVQLQQPGELVYKPGASVKISCKASGYTFSTYMMHWKQRPQGGLRWIGRIYDGDSDNY 60
 Oy 189 NGKFEKAITLADKSSSTAVYQLSLTSVDSAVYFCARSGILRYANDYMGQGSTVTVSS 247

Db 13 GTAGVQCQVQLQDSGPELVKPGASVKISCKASGYTFSTYIHWKQRPQGGLRWIGIYIP 72
 Oy 182 GDGSSNNGKFEKAITLADKSSSTAVYQLSLTSVDSAVYFCARSGILRYANDYMGQGT 241
 Db 73 GDGNTKYNKFKGKTTLADKSSSTAVYQLSLTSVDSAVYFCARSGILRYANDYMGQGT 130
 Oy 242 SVTVSS 247
 Db 131 TLTVSS 136

RESULT 9
 ID Q924Q6 PRELIMINARY; PRT; 145 AA.
 AC Q924Q6;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE VH186.2-D-U-C mu protein (fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6;
 RA Kozono Y., Kozono H., Azuma T.,
 RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
 RT Affinity Maturation of B Cell Antigen Receptors in Response to (4-
 RT Hydroxy-3-Nitrophenyl)Acetyl (NP)."
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB067794; BAB63279.1; -
 DR PIR; F28833; F28833.
 DR PIR; F33932; F33932.
 DR PIR; PH1105; PH1105.
 DR PIR; PH1108; PH1108.
 DR PIR; PH1114; PH1114.
 DR PIR; PH1118; PH1118.
 DR PIR; PH1119; PH1119.
 DR PIR; PH1125; PH1125.
 DR PIR; PH1126; PH1126.
 DR PIR; PH1128; PH1128.
 DR PIR; PH1129; PH1129.
 DR PIR; PH1131; PH1131.
 DR PIR; PH1134; PH1134.
 DR PIR; PH1137; PH1137.
 DR PIR; PH1139; PH1139.
 DR PIR; PH1142; PH1142.
 DR PIR; PH1144; PH1144.
 DR PIR; PH1147; PH1147.
 DR PIR; PH1149; PH1149.
 DR PIR; PH1150; PH1150.
 DR PIR; PH1151; PH1151.
 DR PIR; PH1152; PH1152.
 DR PIR; PH1153; PH1153.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig_1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PSS0835; IG_LIKE; 1.
 FT NON_TER
 FT NON_TER
 SQ SEQUENCE 145 AA; 16011 MW; 9BC0846D40DF972EA CRC64;

Query Match 35.6%; Score 469.5; DB 11; Length 145;
 Best Local Similarity 76.7%; Pred. No. 4.6e-32;
 Matches 92; Conservative 7; Mismatches 20; Indels 1; Gaps 1;
 Oy 129 EVQLQDSGPELVKPGASVKISCKDQGYAFNNSMMNWVKQRPQGGLRWIGRIYDGDSDNY 188
 Db 1 QVQLQQPGELVYKPGASVKISCKASGYTFSTYMMHWKQRPQGGLRWIGRIYDGDSDNY 60
 Oy 189 NGKFEKAITLADKSSSTAVYQLSLTSVDSAVYFCARSGILRYANDYMGQGSTVTVSS 247

Db 61 NEKFSKATLTVDKSSSTAYMQLSSLTSDSASVYCCASTLSHYYAMDMYGQGSTVTVSS 120

RESULT 10

ID Q92409 PRELIMINARY; PRT; 145 AA.

AC Q92409; 01-DEC-2001 (TREMblrel. 19, Created)
 DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
 DT 01-OCT-2003 (TREMblrel. 25, Last annotation update)
 DE VH186.2-D-J-C mu protein (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN=CS7BL/6;
 RA Kozono Y., Kozono H., Azuma T.;
 RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
 Affinity Maturation of B Cell Antigen Receptors in Response to (4-
 Hydroxy-3-Nitrophenyl)Acetyl (NP)."
 RL Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB067791; BAB63276.1; -

DR PIR; F28833; F28833.
 DR PIR; F33932; F33932.
 DR PIR; PH105; PH105.
 DR PIR; PH108; PH108.
 DR PIR; PH114; PH114.
 DR PIR; PH118; PH118.
 DR PIR; PH119; PH119.
 DR PIR; PH125; PH125.
 DR PIR; PH126; PH126.
 DR PIR; PH128; PH128.
 DR PIR; PH129; PH129.
 DR PIR; PH131; PH131.
 DR PIR; PH134; PH134.
 DR PIR; PH137; PH137.
 DR PIR; PH139; PH139.
 DR PIR; PH142; PH142.
 DR PIR; PH144; PH144.
 DR PIR; PH147; PH147.
 DR PIR; PH149; PH149.
 DR PIR; PH150; PH150.
 DR PIR; PH151; PH151.
 DR PIR; PH152; PH152.
 DR PIR; PH153; PH153.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig_1.
 DR SMART; SMO0406; IGV_1.
 DR PROSITE; PSS0835; IG_LIKE; 1.
 FT NON_TER 1
 FT 145
 SQ SEQUENCE 145 AA; 16001 MW; 0F409E809FA33D2 CRC64;

Query Match 35.3%; Score 465.5; DB 11; Length 145;
 Best Local Similarity 75.8%; Pred. No. 1e-31;
 Matches 91; Conservative 8; Mismatches 20; Indels 1; Gaps 1;

QY 129 EVOLQSGPELVKPGASVKISCKDGYAFNSSMMWVKRPPGQGLEMTGIRITPGGDSNY 188
 DB 1 QVQLQPGAEVLVPGASVKISCKASGYTFTSYMMHWVKRPPGGLGWIGRIDPNSGGTKY 60

QY 189 NGKFEKAILTADKSSSTAYMQLSSLTSDSASVYFCARGLR-YAMDYMGQGSTVTVSS 247
 DB 61 NEKFSKATLTVDKSSSTAYMQLSSLTSDSASVYCARSLITTYAMDMYGQGSTVTVSS 120

RESULT 11

ID Q924R1 PRELIMINARY; PRT; 145 AA.

AC Q924R1; 01-DEC-2001 (TREMblrel. 19, Created)

DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
 DT 01-OCT-2003 (TREMblrel. 25, Last annotation update)
 DE VH186.2-D-J-C mu protein (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN=CS7BL/6;
 RA Kozono Y., Kozono H., Azuma T.;
 RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
 Affinity Maturation of B Cell Antigen Receptors in Response to (4-
 Hydroxy-3-Nitrophenyl)Acetyl (NP)."
 RL Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB067789; BAB63274.1; -

DR PIR; F28833; F28833.
 DR PIR; F33932; F33932.
 DR PIR; PH105; PH105.
 DR PIR; PH108; PH108.
 DR PIR; PH114; PH114.
 DR PIR; PH118; PH118.
 DR PIR; PH119; PH119.
 DR PIR; PH125; PH125.
 DR PIR; PH126; PH126.
 DR PIR; PH128; PH128.
 DR PIR; PH129; PH129.
 DR PIR; PH131; PH131.
 DR PIR; PH134; PH134.
 DR PIR; PH137; PH137.
 DR PIR; PH139; PH139.
 DR PIR; PH142; PH142.
 DR PIR; PH144; PH144.
 DR PIR; PH147; PH147.
 DR PIR; PH149; PH149.
 DR PIR; PH150; PH150.
 DR PIR; PH151; PH151.
 DR PIR; PH152; PH152.
 DR PIR; PH153; PH153.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig_1.
 DR SMART; SMO0406; IGV_1.
 DR PROSITE; PSS0835; IG_LIKE; 1.
 FT NON_TER 1
 FT 145
 SQ SEQUENCE 145 AA; 15979 MW; 0162D0A26C746C04 CRC64;

Query Match 35.3%; Score 464.5; DB 11; Length 145;
 Best Local Similarity 75.8%; Pred. No. 1.2e-31;
 Matches 91; Conservative 7; Mismatches 21; Indels 1; Gaps 1;

QY 129 EVOLQSGPELVKPGASVKISCKDGYAFNSSMMWVKRPPGQGLEMTGIRITPGGDSNY 188
 DB 1 QVQLQPGAEVLVPGASVKISCKASGYTFTSYMMHWVKRPPGGLGWIGRIDPNSGGTKY 60

QY 189 NGKFEKAILTADKSSSTAYMQLSSLTSDSASVYFCAR-GLR-YAMDYMGQGSTVTVSS 247
 DB 61 NEKFSKATLTVDKSSSTAYMQLSSLTSDSASVYCARISGFAYAMDMYGQGSTVTVSS 120

RESULT 12

ID Q924R4 PRELIMINARY; PRT; 145 AA.

AC Q924R4; 01-DEC-2001 (TREMblrel. 19, Created)
 DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
 DT 01-OCT-2003 (TREMblrel. 25, Last annotation update)
 DE VH186.2-D-J-C mu protein (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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Query	Best Local Similarity	Score	DB	Length
Matches 91; Conservative 7; Mismatches 21; Indels 1; Gaps 1				
Qy 129 EVOLQSGPELVKPGASVYISCKDSCYAFNSGMNWNVQKQPGQGLEWIGRIYPGQGSNY 188				
Db 1 QVQLQDQGLAVLPKPGASVYLSCKASGYPTFSYMMHWVQKQPGRGLEWIGRIDPNSGGTKY 60				
Qy 189 NGKPEGAITLTAKSSSTAYMOLSLTSDSAVYFCASGL-LVANDYWGCGSYTVSS 247				
Db 61 NEFKSKATITVDKPSSTAYMOLSLTSDSAVYFCASDPDYDIADMYGCGSYTVSS 120				

```

RT "humanized porcine VCAW-specific monoclonal antibodies with chimeric
RT EGG2/G4 constant regions block human leukocyte binding to porcine
RT endothelial cells."
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
DR HSBP; P01810; 2FBJ.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG_1.
DR SMART; SM00406; IGV_1.
DR PROSITE; PSS0835; IG_LIKE; 1.
DR NON_TER
FT NON_TER
FT TER
SQ SEQUENCE 118 AA; 13036 MW; 90EBC59D31ECAFCC CRC64;

Query Match 35.2%; Score 463.5; DB 11; Length 118;
Best Local Similarity 74.8%; Pred. No. 1,1e-31;
Matches 89; Conservative 10; Mismatches 19; Indels 1; Gaps 1

QY 129 EVVLQSGEELVYPASVKIKCKSGIAFNSSMMWNTKQSPGGGLEWIGHITIPGCDNSY 188
Db 1 QVAVQSGSEELRPAASVKIKCKSGIAFNSSMMWNTKQSPGGGLEWIGHITIPGCDNSY 60

QY 189 NGKFEKALITLADKSSATYMOISLTSVDSAYVFCARSGILRYADPDYMQGTSVTSS 247
Db 61 TQKFRKALITLADKSSATYMOISLTSVDSAYVFCARSRVGSY-PDYMQGITLTVSS 118

RESULT 14
QSR062 PRELIMINARY; PRT; 234 AA.
AC QSR062;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
DE Mus musculus (mouse).
OC Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus;
OX NCBI_Taxid=10090;
[1]
SEQUENCE FROM N.A.
RA Strausberg R.;
RC TISSUE=Colon;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC027418; AAH27418.1;
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG_2.
DR SMART; SM00406; IGV_1.
DR PROSITE; PSS0835; IG_LIKE; 2.
DR PROSITE; PSS0280; IG_MHC; 1.
DR KW Hypothetical protein.
SQ SEQUENCE 234 AA; 25857 MW; 4EB08C81426AEAB1 CRC64;

Query Match 35.1%; Score 462.5; DB 11; Length 234;
Best Local Similarity 48.0%; Pred. No. 3,3e-31;
Matches 107; Conservative 13; Mismatches 52; Indels 51; Gaps 4

QY 1 DIOMOTTSLSASIGDRAVTVSCASODIRMYLWVWQKQKPDGVTKPLIYTSLSLQGVSS 60
Db 21 DIOMOTTSLSASIGDRAVTVSCASQGISNYLWVWQKQKPDGVTKPLIYTSLSHGVSS 80

QY 61 RFGSGSGTDVSLITINLNEQEDIGTFPCQGNTPPMTFGGGTXKLEIKRGGGSGDGSGSG 120
Db 81 RFGSGSGTHYSLITINLEPEDIAIYVCOQYSCPFPGFGGTXKLEIKR----- 128

QY 121 GSGGGGGSEVQLQGGPELVKPGASVKIKSCDSDSYAHSMMWNTKQSPGGGLEWIGHIT 180
Db 129 --ADAAPTISIPPSSEQLTSGASV-----VCFINNFY 160

QY 181 PG-----DGDSDNYNGKFEKALITLADKSSATYMOISLTT 215

```


GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 22, 2004, 11:48:48 ; Search time 10.5 Seconds
(without alignments)
1224.888 Million cell updates/sec

Title: US-10-620-049-23

Perfect score: 1317

Sequence: 1 DIQMTQTSSLSASIGDRVT.....GLRYAMDYWGQSTVTVSS 247

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	511	38.8	108	1	KV5K_MOUSE
2	510	38.7	108	1	KV5N_MOUSE
3	509	38.6	108	1	KV5L_MOUSE
4	501	38.0	108	1	KV5O_MOUSE
5	497	37.7	108	1	KV5K_MOUSE
6	476	36.1	108	1	KV5U_MOUSE
7	453	34.7	108	1	KV5U_MOUSE
8	447	34.6	108	1	KV5O_MOUSE
9	440.5	33.4	139	1	HV07_MOUSE
10	430	32.6	120	1	HV03_MOUSE
11	426.5	32.4	137	1	HV11_MOUSE
12	423	32.1	117	1	HV52_MOUSE
13	421	32.0	117	1	HV06_MOUSE
14	419	31.8	138	1	HV48_MOUSE
15	415	31.5	117	1	HV13_MOUSE
16	414	31.4	121	1	HV01_MOUSE
17	413	31.4	117	1	HV12_MOUSE
18	406.5	30.9	118	1	HV51_MOUSE
19	405	30.8	117	1	HV05_MOUSE
20	403	30.6	117	1	HV04_MOUSE
21	400.5	30.4	120	1	HV50_MOUSE
22	395	30.0	108	1	KV5P_MOUSE
23	394	29.9	108	1	KV1Y_HUMAN
24	392	29.8	130	1	KV5G_MOUSE
25	388	29.5	117	1	HV09_MOUSE
26	386	29.3	108	1	KV1O_HUMAN
27	384	29.2	108	1	KV1A_HUMAN
28	383	29.1	108	1	KV1R_HUMAN
29	382	29.0	117	1	HV49_MOUSE
30	381	28.9	108	1	KV1P_HUMAN
31	379	28.8	117	1	HV10_MOUSE
32	377	28.6	117	1	HV14_MOUSE

34	372	28.2	129	1	KV1W_HUMAN	P04431 homo sapien
35	371	28.2	108	1	KV1S_HUMAN	P01611 homo sapien
36	369	28.0	108	1	KV1M_HUMAN	P01605 homo sapien
37	369	28.0	108	1	KV1O_HUMAN	P01609 homo sapien
38	368	27.9	108	1	KV1E_HUMAN	P01597 homo sapien
39	368	27.9	108	1	KV1H_HUMAN	P01600 homo sapien
40	368	27.9	108	1	KV1G_HUMAN	P04430 homo sapien
41	367	27.9	108	1	KV1G_HUMAN	P01599 homo sapien
42	366	27.8	108	1	KV1C_HUMAN	P01595 homo sapien
43	362	27.5	128	1	KV5E_MOUSE	P01637 mus musculu
44	362	27.5	136	1	HV15_MOUSE	P01759 mus musculu
45	361	27.4	108	1	KV1L_HUMAN	P01604 homo sapien

ALIGNMENTS

RESULT 1	ID	KV5K_MOUSE	STANDARD	PRT	108 AA.
AC	P01644				
DT	21-JUL-1986 (Rel. 01, Created)				
DT	21-JUL-1986 (Rel. 01, Last sequence update)				
DT	28-FEB-2003 (Rel. 41, Last annotation update)				
DE	Ig kappa chain V-V region HP R16.7.				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
OX	NCBI_TaxID=10090;				
RN	[1]				
RP	SEQUENCE.				
RC	STRAIN=A/T;				
RA	MEDLINE=82150934; PubMed=6801658;				
RT	Siegalman M., Capra J.D.;				
RT	"Complete amino acid sequence of light chain variable regions derived				
RT	from five monoclonal anti-p-azophenylarsenate antibodies differing				
RT	with respect to a crossreactive idiotype."				
RU	Proc. Natl. Acad. Sci. U.S.A. 78:7679-7683(1981).				
CC	-I- MISCELLANEOUS: Anti-arsenate hydriodoma protein.				
DR	PIR; A01927; KIMSAR.				
DR	HSSP; P01607; IREI.				
DR	InterPro; IPR007110; Ig-like.				
DR	InterPro; IPR003596; Ig_V.				
DR	Pfam; PF00047; Ig; 1.				
DR	SMART; SMO0406; IgV; 1.				
DR	PROSITE; PS50835; IG LIKE; 1.				
KM	Immunoglobulin V region.				
FT	DOMAIN 1 23				FRAMEWORK-1.
FT	DOMAIN 24 34				COMPLEMENTARITY-DETERMINING-1.
FT	DOMAIN 35 49				FRAMEWORK-2.
FT	DOMAIN 50 56				COMPLEMENTARITY-DETERMINING-2.
FT	DOMAIN 57 88				FRAMEWORK-3.
FT	DOMAIN 89 97				COMPLEMENTARITY-DETERMINING-3.
FT	DOMAIN 98 108				FRAMEWORK-4.
FT	DISULFID 23 88				BY SIMILARITY.
FT	NON TER 108 108				
SC	SEQUENCE 108 AA; 11910 MW; A55464263EFP597 CRC64;				
Query Match					
Best Local Similarity 90.7%; Score 511; DB 1; Length 108;					
Matches 98; Conservative 3; Mismatches 7; Indels 0; Gaps 0;					
QY	1	DIQMTQTSSLSASIGDRVTSCRASQDIRNYLWYQCKPGTYKFLYYTSRLQPGVPS 60			
DB	1	DIQMTQTSSLSASIGDRVTISCRASQDISYLMWYQCKPGTYKFLYYTSRLHSGVPS 60			
QY	61	RFGSGSGSDYSLTINNEQEDIGYFPCQGNLPTWPGGQTKLEIKR 108			
DB	61	RFGSGSGSDYSLTINNEQEDIGYFPCQGNLPTWPGGQTKLEIKR 108			

Matches 96; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 1 DIQMTQTSSISASLGRTVWSCASQDINRYLNWYQKPGDGYKFLIYTSRLQPGVPS 60
 DB 1 DIQMTQTSSISASLGRTVWSCASQDINRYLNWYQKPGDGYKFLIYTSRLHSGVPS 60
 QY 61 RFSGSGSGTDYSLTINLEQEDIGTYFCQCGNTPPWTFGGGTKEIKR 108
 DB 61 RFSGSGSGTDYSLTINLEQEDIGTYFCQCGNTPPWTFGGGTKEIKR 108

RESULT 5

KV5M_MOUSE STANDARD; PRT; 108 AA.

ID KV5M_MOUSE
 AC P01643;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Ig kappa chain V-V region HP 12356.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CC NCBI_Taxid=10090;
 RN [1]

RA SRAIN=A/U;
 RX MEDLINE=82150934; PubMed=6801658;
 RT "Complete amino acid sequence of light chain variable regions derived from five monoclonal anti-P-azophenylarsenate antibodies differing with respect to a crossreactive idiotype."
 RL Proc. Natl. Acad. Sci. U.S.A. 78:7679-7683(1981).
 CC -1- MISCELLANEOUS: Anti-arsenate hybridoma protein.
 DR HSP; P01607; IREI.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SMO0406; IgV; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 DR Immunoglobulin V region.
 KW DOMAIN 1 23
 FT DOMAIN 1 23
 FT DOMAIN 24 34
 FT DOMAIN 35 49
 FT DOMAIN 50 56
 FT DOMAIN 57 88
 FT DOMAIN 89 97
 FT DOMAIN 98 108
 FT DISULFID 23 88
 FT NON_TER 108
 SQ SEQUENCE 108 AA; 11989 MW; 4C98599C08BEA09A CRC64;

Query Match 37.7%; Score 497; DB 1; Length 108;
 Best Local Similarity 88.9%; Pred. No. 6,5e-33;
 Matches 96; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 1 DIQMTQTSSISASLGRTVWSCASQDINRYLNWYQKPGDGYKFLIYTSRLQPGVPS 60
 DB 1 DIQMTQTSSISASLGRTVWSCASQDINRYLNWYQKPGDGYKFLIYTSRLHSGVPS 60
 QY 61 RFSGSGSGTDYSLTINLEQEDIGTYFCQCGNTPPWTFGGGTKEIKR 108
 DB 61 RFSGSGSGTDYSLTINLEQEDIGTYFCQCGNTPPWTFGGGTKEIKR 108

RESULT 6

KV5U_MOUSE STANDARD; PRT; 108 AA.

ID KV5U_MOUSE
 AC P04946;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-V region NOS-89.4.
 OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CC NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=83271467; PubMed=6877353;
 RA Kaartinen M., Griffiths G.M., Markham A.F., Milstein C.;
 RT "RNA sequences define an unusually restricted IgG response to 2-phenylloxazalone and its early diversification."
 RL Nature 304:320-324(1983).
 CC -1- MISCELLANEOUS: ANTI-2-PHENYL OXAZOLONE (PHOX) ANTIBODY.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
 CC -----

CC EMBL; K00745; AAA38690.1; -.
 DR HSP; P01607; IREI.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SMO0406; IgV; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 DR Immunoglobulin V region; Hybridoma.
 KW DOMAIN 1 23
 FT DOMAIN 1 23
 FT DOMAIN 24 34
 FT DOMAIN 35 49
 FT DOMAIN 50 56
 FT DOMAIN 57 88
 FT DOMAIN 89 97
 FT DOMAIN 98 107
 FT DISULFID 23 88
 FT NON_TER 108
 SQ SEQUENCE 108 AA; 11866 MW; DB2C885920DC6DD CRC64;

Query Match 36.1%; Score 476; DB 1; Length 108;
 Best Local Similarity 84.3%; Pred. No. 2.7e-30;
 Matches 91; Conservative 4; Mismatches 13; Indels 0; Gaps 0;

QY 1 DIQMTQTSSISASLGRTVWSCASQDINRYLNWYQKPGDGYKFLIYTSRLQPGVPS 60
 DB 1 DIQMTQTSSISASLGRTVWSCASQDINRYLNWYQKPGDGYKFLIYTSRLHSGVPS 60
 QY 61 RFSGSGSGTDYSLTINLEQEDIGTYFCQCGNTPPWTFGGGTKEIKR 108
 DB 61 RFSGSGSGTDYSLTINLEQEDIGTYFCQCGNTPPWTFGGGTKEIKR 108

RESULT 7
 KV5U_MOUSE STANDARD; PRT; 108 AA.
 ID KV5U_MOUSE
 AC P01643;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-V region MOPC 173.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CC NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=76091934; PubMed=812636;
 RA Schiff C., Fougereau M.;
 RT "Determination of the primary structure of a mouse IgG2a immunoglobulin. Amino-acid sequence of the light chain."
 RL Eur. J. Biochem. 59:525-537(1975).
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
 DR PIR; A01926; KMS73.

DR HSPB, P01607, 1REI. Ig-like.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003596; Ig_v.
 DR Pfam: PF00047; Ig; 1.
 DR SMART: SM00406; IGV; 1.
 DR PROSITE: PS50835; IG LIKE; 1.
 DR Immunoglobulin V region.
 KM DOMAIN 1 23 FRAMEWORK-1.
 FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 35 49 FRAMEWORK-2.
 FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 57 88 FRAMEWORK-3.
 FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
 FT DOMAIN 98 108 FRAMEWORK-4.
 FT DISULFID 23 88 BY SIMILARITY.
 FT NON_TER 108 108
 SQ SEQUENCE 108 AA; 11819 MW; 2AD29D92A72A0A3 CRC64;

Query Match 34.7%; Score 457; DB 1; Length 108;
 Best Local Similarity 79.6%; Pred. No. 7.8e-29;
 Matches 86; Conservative 9; Mismatches 13; Indels 0; Gaps 0;

QY 1 DIQNTQTSSLSASLGPRVYSCASODIRNYLNMVYQKPDGYKFLITYTSKLGCVS 60
 DB 1 DIQNTQTSSLSASLGPRVYSCASODIRNYLNMVYQKPDGYKFLITYTSKLGCVS 60
 QY 61 RFSGSGSTGYSLTINNLECEIDIGTFCQOQNPPTFGGTGKLEIKR 108
 DB 61 RFSGSGSTGYSLTINNLECEIDIGTFCQOQNPPTFGGTGKLEIKR 108

RESULT 8
 ID HV02_MOUSE STANDARD; PRT; 140 AA.
 AC P01746;
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Ig heavy chain V region 9367 precursor.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NC NCB1_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A/J;
 RX MEDLINE=82152818; PubMed=6801765;
 RA Sline U., Rablites T.H., Estess P., Slaughter C., Tucker P.W.,
 RA Capra J.D.;
 RT "Somatic mutation in genes for the variable portion of the
 RT immunoglobulin heavy chain."
 RL Science 246:309-311(1982).
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.

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 CC or send an email to license@isb-sdb.ch).
 CC -----
 CC EMBL: J00493; AAA8128.1; -.
 DR PIR: A94264; HVMSG7.
 DR HSPB: P01610; 2FRF.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003596; Ig_v.
 DR Pfam: PF00047; Ig; 1.
 DR SMART: SM00406; IGV; 1.
 DR PROSITE: PS50835; IG LIKE; 1.
 DR Immunoglobulin V region; Hybridoma; Signal.
 FT SIGNAL 1 19
 FT CHAIN 20 140 IG HEAVY CHAIN V REGION 9367.

FT DOMAIN 20 139 IG-LIKE.
 FT NON_TER 140 140
 SQ SEQUENCE 140 AA; 15514 MW; 25A4CBBE31DA5C88 CRC64;
 Query Match 33.6%; Score 443; DB 1; Length 140;
 Best Local Similarity 70.9%; Pred. No. 1.2e-27;
 Matches 90; Conservative 8; Mismatches 27; Indels 2; Gaps 1;

QY 123 SGGGSEVQLQSGPELYKPGASVKISCKDGYAFNNSMMWYQKPGQGLEMTGRITPQ 182
 DB 14 TAGHSEVQLQSGPELYKPGASVKISCKDGYAFNNSMMWYQKPGQGLEMTGRITPQ 73
 QY 183 DGDSSNYGKPFEGKAILTLADKSSSTAYMQLSLTSVDSAVYFCARSGLL--RYAMDYWGQG 240
 DB 74 NGYINYNKPFKQKTLTLVDKSSSTAYMQLSLTSVDSAVYFCARSGLL--RYAMDYWGQG 133
 QY 241 TSVTVSS 247
 DB 134 TPLTVSS 140

RESULT 9
 ID HV07_MOUSE STANDARD; PRT; 139 AA.
 AC P01751; P01752;
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Ig heavy chain V region B1-8/186-2 precursor.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NC NCB1_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6;
 RX MEDLINE=81234548; PubMed=6788376;
 RA Botwell A.L.M., Parkind M., Keth M., Tanishi-Kari T., Rajewsky K.,
 RA Baltimore D.;
 RT "Heavy chain variable region contribution to the Npb family of
 RT antibodies: somatic mutation evident in a gamma 2a variable region."
 RL Cell 24:625-637(1981).
 CC -1- MISCELLANEOUS: THE B1-8 MU CHAIN MRNA WAS CLONED FROM A HYBRIDOMA
 CC MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
 CC (NPB ANTIBODIES).
 CC -----

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 CC -----
 CC EMBL: J00529; AAA8170.1; -.
 DR PIR: A90809; MEMS18.
 DR PDB: 1AEU; 27-MAY-98.
 DR PDB: 1A6W; 15-JUL-98.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003596; Ig_v.
 DR Pfam: PF00047; Ig; 1.
 DR SMART: SM00406; IGV; 1.
 DR PROSITE: PS50835; IG LIKE; 1.
 DR Immunoglobulin V region; Signal; 3D-structure.
 FT SIGNAL 1 19
 FT CHAIN 20 139 IG HEAVY CHAIN V REGION B1-8/186-2.
 FT DOMAIN 20 49 FRAMEWORK-1.
 FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 55 68 FRAMEWORK-2.
 FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 86 117 FRAMEWORK-3.
 FT DOMAIN 118 124 D SEGMENT.
 FT DOMAIN 125 139 JH2 SEGMENT.

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FT DISULFID 41 115 BY SIMILARITY.
FT NON TER 139 139
SQ SEQUENCE 139 AA; 15419 MW; 1B57DD4FD0C9F465 CRC64;

Query Match
Best Local Similarity 33.4%; Score 440.5; DB 1; Length 139;
Matches 87; Conservative 10; Mismatches 26; Indels 1; Gaps 1;

QY 135 GGGSEVQLQSGPELVKPGASVKISCKDGYAFNNSMMNWYKORPGGLEWIGRIYPDG 184
DB 16 GVHSGVQLQSGPELVKPGASVKISCKDGYAFNNSMMNWYKORPGGLEWIGRIYPDG 75
QY 185 DSNYNGKFEKALITLADKSSSTAYNQSLTSVDSAVYFCARSGLLRYA-MDYMGQGTSTV 243
DB 76 GTRVNEKFSKATLTVDKPSSTAYNQSLTSVDSAVYFCARSGLLRYA-MDYMGQGTSTL 135
QY 244 TVSS 247
DB 136 TVSS 139

RESULT 10
HV03_MOUSE STANDARD; PRT; 120 AA.
ID HV03_MOUSE
AC P01747;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE IG heavy chain V region 36-65.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RP SEQUENCE FROM N.A.
RX MEDLINE=83131846; PubMed=6166498;
RA Stekevitz M., Gelfer M.L., Brodeur P., Riblet R.,
RA Marshak-Rothstein A.;
RT "The genetic basis of antibody production: the dominant anti-arsenate
RT idiotype response of the strain A mouse.";
RL Eur. J. Immunol. 12:1023-1032(1982).
CC -1- MISCELLANEOUS: FROM ANALYSIS OF THE SIZES OF SEVERAL OTHER
CC DIFFERENTIATED GENES THAT HYBRIDIZE TO THIS ONE, THE AUTHORS
CC CONCLUDE THAT ALL OF THESE V REGIONS HAVE REARRANGED TO THE SAME J
CC SEGMENT, JH2.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR HSSP; P01789; IMCP.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Ig; 1.
DR PROSITE; PS50835; IG-LIKE; 1.
FT DOMAIN 1 111
FT NON TER 120
SQ SEQUENCE 120 AA; 13307 MW; FF04E4A167B654AF CRC64;

Query Match
Best Local Similarity 32.6%; Score 430; DB 1; Length 120;
Matches 86; Conservative 9; Mismatches 23; Indels 2; Gaps 1;

QY 130 VOIQSGPELVKPGASVKISCKDGYAFNNSMMNWYKORPGGLEWIGRIYPDGDSNTN 189
DB 1 VOIQSGPELVKPGASVKISCKDGYAFNNSMMNWYKORPGGLEWIGRIYPDGDSNTN 60
QY 190 GKEEGKALITLADKSSSTAYNQSLTSVDSAVYFCARSGLL--RYANDYMGQGTSTVSS 247
DB 61 EKFGKTLTVDKSSSTAYNQSLTSVDSAVYFCARSGLL--RYANDYMGQGTSTLTVSS 120

RESULT 11
HV11_MOUSE STANDARD; PRT; 137 AA.
ID HV11_MOUSE

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AC P01755;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG heavy chain V region 543 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RP SEQUENCE FROM N.A.
RX MEDLINE=81234548; PubMed=6788376;
RA Bochwella A.L.M., Paskind M., Rech M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NpB family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -1- MISCELLANEOUS: THE GAMMA-2A CHAIN WEA WAS CLONED FROM A HYBRIDOMA
CC MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
CC (NPB ANTIBODIES).
CC -----
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CC or send an email to license@sb-sib.ch).
CC -----
DR EMBL; J00539; AAA8172.1; -.
DR PIR; A02038; GZMS43.
DR HSSP; P01810; 2FBU.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Ig; 1.
DR PROSITE; PS50835; IG-LIKE; 1.
KM Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 137
FT DOMAIN 20 49
FT DOMAIN 50 54
FT DOMAIN 55 68
FT DOMAIN 69 85
FT DOMAIN 86 117
FT DOMAIN 118 122
FT DOMAIN 123 137
FT DISULFID 41 115
FT NON TER 137
SQ SEQUENCE 137 AA; 15200 MW; ADD5881BF448BEC9 CRC64;

Query Match
Best Local Similarity 32.4%; Score 426.5; DB 1; Length 137;
Matches 86; Conservative 8; Mismatches 28; Indels 1; Gaps 1;

QY 125 GGGSEVQLQSGPELVKPGASVKISCKDGYAFNNSMMNWYKORPGGLEWIGRIYPDG 184
DB 16 GVHSGVQLQSGPELVKPGASVKISCKDGYAFNNSMMNWYKORPGGLEWIGRIYPDG 75
QY 185 DSNYNGKFEKALITLADKSSSTAYNQSLTSVDSAVYFCARSGLLRYANDYMGQGTSTV 244
DB 76 GTTVNEHRRSKATLTVDKPSSTAYNQSLTSVDSAVYFCARSGLLRYANDYMGQGTSTL 134
QY 245 VSS 247
DB 135 VSS 137

RESULT 12
HV52_MOUSE STANDARD; PRT; 117 AA.
ID HV52_MOUSE
AC P06327;
DT 01-JAN-1988 (Rel. 06, Created)

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DT 01-JAN-1988 (Rel. 06, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region VH558 A1/A4 precursor.
OS Mus musculus (Mouse).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Euteleia; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=8509340; PubMed=2578321;
RA Yancopoulos G.D., Alt P.W.;
RT "Developmentally controlled and tissue-specific expression of
RL Cell 40:271-281 (1985).
CC -----
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CC -----
CC
CC EMBL; M13787; AAA8499.1; -.
CC DR PIR; A02029; HVM5A1.
CC DR HSSP; P01810; 2F8J.
CC DR InterPro; IPR007110; IG-like.
CC DR InterPro; IPR003596; IG_.
CC Pfam; PF00047; Ig_1.
CC SMART; SM00406; IGV; 1.
CC DR PROSITE; PSS0835; IG_LIKE; 1.
CC KW Immunoglobulin V region; Signal.
CC FT SIGNAL 1 19
CC FT CHAIN 20 117 IG HEAVY CHAIN V REGION VH558 A1/A4.
CC FT DOMAIN 20 49 FRAMEWORK-1.
CC FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
CC FT DOMAIN 55 68 FRAMEWORK-2.
CC FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
CC FT DOMAIN 86 117 FRAMEWORK-3.
CC FT DISULFID 41 115 BY SIMILARITY.
CC FT NON TER 117
CC SQ SEQUENCE 117 AA; 12971 MW; 830BC138856DFC9D CRC64;
Query Match 32.1%; Score 423; DB 1; Length 117;
Best Local Similarity 79.0%; Pred No. 3.5e-26;
Matches 83; Conservative 6; Mismatches 16; Indels 0; Gaps 0
Cy 122 GSGGGSEYVOIQSGPELVKPGASVYKISKDGYAFNSSWMNVKRPQGGLEWIGRIYP 181
Db 13 GTAGVHCQVOIQSGPELVKPGALVKISKAGYFTSDIMVWQRPQGGLEWIGRIYP 72
Cy 182 GDGSDNVNGKPEGKAILTPADKSSPAYMQLSLTSVDSAVYFCAR 226
Db 73 GDGSKTNEKFKKAILTPADKSSPAYMQLSLTSVDSAVYFCAR 117
RESULT 13
ID HV06 MOUSE STANDARD; PRT; 117 AA.
AC P01750;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region 102 precursor.
OS Mus musculus (Mouse).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Euteleia; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=8134548; PubMed=6786376;
RA Botwell A.L.W., Paekind M., Reith M., Imanishi-Kari T., Rajewsky K.,

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RA	Baltimore D.; heavy chain variable region contribution to the NpB family of antibodies; somatic mutation evident in a gamma 2a variable region.";
RL	Cell 24:625-637(1981).
CC	-1- MISCELLANEOUS. THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY RELATED GENES THAT COULD ENCODE V REGIONS OF NPb ANTIBODIES.
DR	FIR; A02032; HVMS02.
DR	HSSP; P01810; 2FBJ.
DR	Interpro; IPR007110; IG-1like.
DR	Interpro; IPR003596; Ig_v.
DR	Pfam; PF00047; Ig_1.
DR	SMART; SMO0406; IGV; 1.
DR	PROSITE; PS50835; IG_LIKE; 1.
KM	Immunoglobulin V region; Signal.
FT	SIGNAL 1 19
FT	CHAIN 20 117
FT	DOMAIN 20 49
FT	DOMAIN 20 49
FT	DOMAIN 50 54
FT	DOMAIN 55 68
FT	DOMAIN 69 85
FT	DOMAIN 86 117
FT	DIGUFID 41 115
FT	NON_TER 117 117
SQ	SEQUENCE 117 AA; 12867 MW; 740A65DD851FCAB8 CEC64;
Oy	Query Match Best Local Similarity 32.0%; Score 421; DB 1; Length 117; Matches 80; Conservative 6; Mismatches 15; Indels 0; Gaps 0
Db	125 GGSGSEYQLQGSEPELVKPSASVVKICKCKSGVFAPNSMMWVKKPPGCGLEWISGIITYGDG 185 16 GVSHSHQLDQPGLVELKPSPASVSKCSKSGYTFTSYNHWKRPKGGLEWIGRIHPSDS 75
Oy	185 DSNYNGKEFGAKILTPADKSSSTAVYNQLSLTSVDSAVFYCA 225 76 DTINYNQFKPKAKLTVDKSSSTAVYNQLSLTSDSAVYYCA 116
Db	RESULT 14 HV48_MOUSE STANDARD; FRT; 138 AA. AC P03980; DT 23-OCT-1986 (Rel. 02, Created) DT 23-OCT-1986 (Rel. 02, Last sequence update) DT 15-JUL-1999 (Rel. 38, Last annotation update) DE Ig heavy chain V region TEPC 1017 precursor. OS Mus musculus (Mouse). OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus. OX NCBI_Taxid=10090; RN [1] RP SEQUENCE FROM N.A. RX MEDLINE=84248078; PubMed=6429663; RA Gilliam A.C., Shen A., Richards J.B., Blattner F.R., Mushinski J.F., Tucker P.M.; "Illegitimate recombination generates a class switch from C mu to C RT delta in an Igd-secreting plasmacytoma."; Proc. Natl. Acad. Sci. U.S.A. 81:4164-4168(1984). RL FIR; A02033; HVMS07. DR HSSP; P01810; 2FBJ. DR Interpro; IPR007110; IG-1like. DR Interpro; IPR003596; Ig_v. DR Pfam; PF00047; Ig_1. DR SMART; SMO0406; IGV; 1. DR PROSITE; PS50835; IG_LIKE; 1. KM Immunoglobulin V region; Signal. FT SIGNAL 1 20 FT CHAIN 21 138 FT DOMAIN 21 49 FT DOMAIN 50 54 FT DOMAIN 55 68 FT DOMAIN 69 85 FT DOMAIN 86 117 IG HEAVY CHAIN V REGION TEPC 1017. FRAMEWORK-1. COMPLEMENTARITY-DETERMINING-1. FRAMEWORK-2. COMPLEMENTARITY-DETERMINING-2. FRAMEWORK-3.

FT DOMAIN 118 127 COMPLEMENTARITY-DETERMINING-3.
 FT DOMAIN 128 138 FRAMEWORK-4.
 FT DISULFID 41 115 BY SIMILARITY.
 FT NON_TER 138 138
 SQ SEQUENCE 138 AA; 15576 MW; 748157E4C6907B8E CRC64;

Query Match 31.8%; Score 419; DB 1; Length 138;
 Best Local Similarity 68.3%; Pred. No. 8.6e-26;
 Matches 82; Conservative 11; Mismatches 27; Indels 0; Gaps 0;

QY 128 SEVQLQSGPELVKPGASVKISCKDGYAFNNSGMNWVKORPGQGLEWIGRIYPGDGSN 187
 DB 19 SCVQLQPGAEIVKPGASVYOLSCKASGHTFTYWIHWVKORPGQGLEWIGRIYNDGRSN 78
 QY 188 YNKEFGKAILTPADKSSSTAYVQSLTSVDSAVYFCARSGILRVAMDYWGQTSVTSS 247
 DB 79 YNKEFGKAILTPADKSSSTAYVQSLTSVDSAVYFCARSGILRVAMDYWGQTSVTSS 138

RESULT 15
 ID HV13 MOUSE STANDARD; PRT; 117 AA.
 AC P01757;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Ig heavy chain V region J558.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_taxid=10090;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=80078170; Pubmed=6765983;
 RA Schilling J., Clevinger B., Davis J.M., Hood L.;
 RT "Amino acid sequence of homogeneous antibodies to dextran and DNA
 RT rearrangements in heavy chain V-region gene segments.";
 RL Nature 283:35-40(1980). SEQUENCES OF 10 HYBRIDOMA PROTEINS THAT ALSO
 CC -1- MISCELLANEOUS: THE SEQUENCES OF 10 HYBRIDOMA PROTEINS THAT ALSO
 CC BIND DEXTRAN DIFFER FROM THAT SHOWN AT 1-7 POSITIONS, MANY OF
 CC WHICH OCCUR IN THE D AND J SEGMENTS.
 CC -1- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
 CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE DOMAIN.
 CC PIR; A26242; MEMSJS.
 DR HESP; P01789; 1MCP.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig_1.
 DR SMART; SM00406; IgV_1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 KM Immunoglobulin V region.
 FT DOMAIN 1 116 IG-LIKE.
 FT DISULFID 22 96 BY SIMILARITY.
 FT NON_TER 117 117
 SQ SEQUENCE 117 AA; 13024 MW; 292E2AF4BE447E41 CRC64;

Query Match 31.5%; Score 415; DB 1; Length 117;
 Best Local Similarity 70.0%; Pred. No. 1.5e-25;
 Matches 84; Conservative 10; Mismatches 22; Indels 4; Gaps 2;

QY 129 EYQLQSGPELVKPGASVKISCKDGYAFNNSGMNWVKORPGQGLEWIGRIYPGDGSN 188
 DB 1 EYQLQSGPELVKPGASVKISCKDGYAFNNSGMNWVKORPGQGLEWIGRIYNDGRSN 60
 QY 189 NGKFEKAILTPADKSSSTAYVQSLTSVDSAVYFCARSGILRVAMDYWGQTSVTSS 247
 DB 61 NGKFEKAILTPADKSSSTAYVQSLTSVDSAVYFCARSGILRVAMDYWGQTSVTSS 117

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OM protein - protein search, using sw model

Run on: April 22, 2004, 11:51:48 ; Search time 14 Seconds
(without alignments)
1697.093 Million cell updates/sec

Title: US-10-620-049-23

Perfect score: 1317
Sequence: 1 DIQMTQTSTSLASLGDRVT.....GLRYAMDYWGQTSVTSS 247

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: p1r78:*
2: p1r7:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	635.5	48.3	287	PC4402	pelB leader/Ig hea
2	542.5	41.2	119	A24672	Ig heavy chain pre
3	529	40.2	108	S69900	Ig kappa chain V r
4	527.5	40.1	117	PL0237	Ig heavy chain V r
5	526	39.9	109	PH0888	Ig kappa chain V r
6	525	39.9	118	PL0231	Ig heavy chain V r
7	525	39.9	122	A29380	Ig kappa chain pre
8	524.5	39.8	117	PL0235	Ig heavy chain V r
9	520	39.5	108	S69903	Ig kappa chain (cl
10	520	39.5	115	JI0080	Ig kappa chain pre
11	519.5	39.4	108	S38862	Ig kappa chain V r
12	518	39.3	126	A34934	Ig kappa chain pre
13	515.5	38.8	117	PL0234	Ig heavy chain V r
14	511.5	38.8	107	S69901	Ig kappa chain (cl
15	511	38.8	108	KVMSAR	Ig kappa chain V r
16	510	38.7	128	A26406	Ig kappa chain V r
17	509.5	38.7	115	PL0238	Ig heavy chain V r
18	508	38.6	108	S19970	Ig kappa chain V r
19	508	38.6	108	S69902	Ig kappa chain (cl
20	507	38.5	108	B26405	Ig kappa chain V r
21	505	38.3	107	B28044	Ig kappa chain V r
22	505	38.3	107	A28044	Ig kappa chain V r
23	503	38.2	108	PL0282	Ig kappa chain V r
24	503	38.2	127	PH1234	Ig kappa chain pre
25	502	38.1	108	C26405	Ig kappa chain V r
26	498.5	37.9	107	S69906	Ig kappa chain (cl
27	488	37.1	107	S32188	Ig kappa chain V r
28	488	37.1	108	S11124	Ig kappa chain V r
29	488	37.1	112	PL0232	Ig heavy chain V r

30	486	36.9	138	2	E32513	Ig heavy chain pre
31	483.5	36.7	140	2	S09216	Ig heavy chain pre
32	483	36.7	107	2	D48677	Ig kappa chain V-J
33	482	36.6	246	2	S38950	Ig gamma chain - m
34	482	36.6	446	2	S40295	Ig gamma-2a chain
35	481	36.5	107	2	B49026	Ig kappa chain V r
36	481	36.5	108	2	B30551	Ig kappa chain V r
37	480	36.4	105	2	PH0087	Ig kappa chain V r
38	480	36.4	111	2	A38740	Ig kappa chain V r
39	475	36.1	109	2	PL0233	Ig heavy chain V r
40	470	35.7	111	2	E38740	Ig kappa chain V r
41	470	35.7	111	2	C38740	Ig kappa chain V r
42	469	35.6	111	2	G38740	Ig kappa chain V r
43	466	35.4	138	2	S21810	Ig heavy chain V r
44	465.5	35.3	120	2	PD0008	Ig heavy chain V r
45	464.5	35.3	120	2	B22769	Ig heavy chain V r

ALIGNMENTS

RESULT 1

PC4402 pelB leader/Ig heavy chain anti-NP/linker type 205/alkaline phosphatase fusion protein

C/Species: Synthetic

C/Date: 06-Nov-1998 #sequence_revision 06-Nov-1998 #text_change 06-Nov-1998

C/Accession: PC4402

R/Suzuki, C.; Ueda, H.; Suzuki, E.; Nagamune, T.

J. Biochem. 122, 322-329, 1997

A/Title: Construction, bacterial expression, and characterization of hapten-specific sir

A/Reference number: PC4402

A/Accession: PC4402

A/Molecule type: DNA

A/Residues: 1-287 <SUZ>

C/Keywords: fusion protein

Query Match 48.3%; Score 635.5; DB 4; Length 287;
Best Local Similarity 53.3%; Pred. No. 4.5e-36;
Matches 138; Conservative 24; Mismatches 82; Indels 15; Gaps 5;

QY	1	DIQMTQT-TSLSASLGDRVTSCRSQ---DINYNLWQOKPDGVKFLIYTSRLQ 56
DB	24	DIQAVTVQESALTTSPGTVTLTCTSSGTAVTSNVMWQEKPDHLFTGLIGSTNRPAP 83
QY	57	GVPSRFGSGSGGTPVSLTNNLEQEDIGTYFCQOQNTPTWTFGGTKLEI-----KRG 109
DB	84	GVPAFSGSLIGDKAALITGAQTEDEALVICALWYSHWVFGGTLTLVSSADAKKD 143
QY	110	GGGSPDGGSGGG 169
DB	144	DAKXDDAKKDDAKDQ---QVLOQPGAEIVKPPASAVLSTCKASGYFTSTYMWKMWVQRP 200
QY	170	GQGLEWIRIRIYVGGDDSNVNGKFEKAILLTADKSSSTAYWQLSSTVSVAIVFCARSG 229
DB	201	GRGLEWIRIRIDPNNGSGTKYNEKFKSKATLTVDKSSSTAYWQLSSTVSVAIVFCAR 260
QY	230	LRVA-MDIWQGTSTVTVSS 247
DB	261	YGSSYFDYWGQGTTLTVSS 279

RESULT 2

A24672 Ig heavy chain precursor V region (VM3-3.2) - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 23-Jul-1999

C/Accession: A24672

R/Winter, E.; Radbruch, A.; Krawinkel, U.

EMBO J. 4, 2861-2867, 1985

A/Reference number: A24672; MUID:86055722; PMID:2998759

A/Accession: A24672

A/Molecule type: DNA

A/Residues: 1-119 <WIN>

A/Cross-references: GB:X03086, NID:G52378, PID:CAA26881.1, PID:G773578
 A/Note: this sequence was determined from the germline gene
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotrimer; immunoglobulin
 F:4-119/Product: Ig heavy chain V region WMD-3.2 #status predicted <MNT>
 F:18-101/Domain: immunoglobulin homology <IMM>

Query Match 41.2%; Score 542.5; DB 2; Length 119;
 Best Local Similarity 85.8%; Pred. No. 3.6e-30;
 Matches 103; Conservative 7; Mismatches 7; Indels 3; Gaps 1;

Qy 128 SEVLOQSGPELVKPGASVYKISCKDSGVAFNSMMWVVKORPGQGLEWIGRIYPGDGSN 187
 Db 3 SQVLOQSGPELVKPGASVYKISCKDSGVAFNSMMWVVKORPGQGLEWIGRIYPGDGTN 62
 Qy 188 YNGKFKGKATLTADKSSSTAYMQLSLTSDSANYFCARSGGLRYANDYGGQTSYVSS 247
 Db 63 YNGKFKGKATLTADKSSSTAYMQLSLTSDSANYFCARD---YGSDDYGGQTTITVSS 119

RESULT 3
 Ig kappa chain (clone KL2.18 / KL4B10 / KL4C11) - mouse
 C/Species: Mus musculus (house mouse)
 C/Date: 14-Feb-1997 #sequence revision 13-Mar-1997 #text_change 21-Jan-2000
 C/Accession: S69900; S69907; S69908
 R/Wislocki, L.J.; Creason, G.; Lehmann, K.R.; Cambier, J.C.
 Immunology 75, 116-121, 1992

A/Title: B-cell proliferation initiated by Ia cross-linking and sustained by interleukin
 A/Reference number: S69900; PMID:92185291; PMID:1537587
 A/Accession: S69900
 A/Status: preliminary; translation not shown
 A/Molecule type: DNA
 A/Residues: 1-108 <WYS>
 A/Cross-references: EMBL:X55041, NID:G511023, PID:CAA38881.1, PID:G511024
 A/Accession: S69907
 A/Status: preliminary; translation not shown
 A/Molecule type: DNA
 A/Residues: 1-108 <WY2>
 A/Cross-references: EMBL:X55048, NID:G511037, PID:CAA38881.1, PID:G511038
 A/Accession: S69908
 A/Status: preliminary; translation not shown
 A/Molecule type: DNA
 A/Residues: 1-108 <WY3>
 A/Cross-references: EMBL:X55049, NID:G511039, PID:CAA38881.1, PID:G511040
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 40.2%; Score 529; DB 2; Length 108;
 Best Local Similarity 92.6%; Pred. No. 2.7e-29;
 Matches 100; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 1 DIQMTQTSSLSASIGDRYVSCRASODIRNYLWYQKPDGTVKFLIYTSRLQGPVS 60
 Db 1 DIQMTQTSSLSASIGDRYVSCRASODIRNYLWYQKPDGTVKFLIYTSRLHSGVPS 60
 Qy 61 RFGSGSGTDYSLTINNLEQEDIGYFCQCGNTPPWTFGGTKLEIKR 108
 Db 61 RFGSGSGTDYSLTINNLEQEDIGYFCQCGNTPPWTFGGTKLEIKR 108

RESULT 4
 PLO231
 Ig heavy chain V region (anti-DNA, 1A11VH) - mouse (fragment)
 C/Species: Mus musculus (house mouse)
 C/Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 16-Aug-1996
 C/Accession: PLO231
 R/Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisevsky, D.; Marshak-Rothstein, A.
 J. Exp. Med. 171, 265-297, 1990
 A/Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic
 A/Reference number: PLO231; PMID:90111618; PMID:2104919
 A/Accession: PLO231
 A/Molecule type: mRNA

A/Residues: 1-117 <SHL>
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotrimer; immunoglobulin
 F:1-30/Region: framework 1
 F:15-98/Domain: immunoglobulin homology <IMM>
 F:31-35/Region: complementarity-determining 1
 F:36-49/Region: framework 2
 F:50-66/Region: complementarity-determining 2
 F:67-98/Region: framework 3
 F:99-109/Region: complementarity-determining 3
 F:110-117/Region: framework 4

Query Match 40.1%; Score 527.5; DB 2; Length 117;
 Best Local Similarity 85.5%; Pred. No. 3.7e-29;
 Matches 100; Conservative 6; Mismatches 10; Indels 1; Gaps 1;

Qy 129 EVLOQSGPELVKPGASVYKISCKDSGVAFNSMMWVVKORPGQGLEWIGRIYPGDGSN 188
 Db 1 QVLOQSGPELVKPGASVYKISCKDSGVAFNSMMWVVKORPGQGLEWIGRIYPGDGTN 60
 Qy 189 NGKFKGKATLTADKSSSTAYMQLSLTSDSANYFCARS-GLIRYANDYGGQTSVT 244
 Db 61 NGKFKGKATLTADKSSSTAYMQLSLTSDSANYFCARARSKTYNDYGGQTSVT 117

RESULT 5
 PH0888
 Ig kappa chain V region (anti-CD3) - mouse (fragment)
 C/Species: Mus musculus (house mouse)
 C/Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 21-Jan-2000
 C/Accession: PH0888
 R/Shalaby, M.R.; Shepard, H.M.; Presta, L.; Rodrigues, M.J.; Beverley, P.C.L.; Feldmann, J.
 J. Exp. Med. 175, 217-225, 1992
 A/Title: Development of humanized bispecific antibodies reactive with cytotoxic lymphocyte
 A/Reference number: PH0888; PMID:92113462; PMID:1346155
 A/Accession: PH0888
 A/Molecule type: mRNA
 A/Residues: 1-109 <SHA>
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: immunoglobulin
 F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 39.9%; Score 526; DB 2; Length 109;
 Best Local Similarity 91.7%; Pred. No. 4.3e-29;
 Matches 99; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 1 DIQMTQTSSLSASIGDRYVSCRASODIRNYLWYQKPDGTVKFLIYTSRLQGPVS 60
 Db 1 DIQMTQTSSLSASIGDRYVSCRASODIRNYLWYQKPDGTVKFLIYTSRLHSGVPS 60
 Qy 61 RFGSGSGTDYSLTINNLEQEDIGYFCQCGNTPPWTFGGTKLEIKR 108
 Db 61 RFGSGSGTDYSLTINNLEQEDIGYFCQCGNTPPWTFGGTKLEIKR 108

RESULT 6
 PLO231
 Ig heavy chain V region (anti-DNA, D20VH) - mouse (fragment)
 C/Species: Mus musculus (house mouse)
 C/Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 16-Aug-1996
 C/Accession: PLO231
 R/Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisevsky, D.; Marshak-Rothstein, A.
 J. Exp. Med. 171, 265-297, 1990
 A/Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic
 A/Reference number: PLO231; PMID:90111618; PMID:2104919
 A/Accession: PLO231
 A/Molecule type: mRNA
 A/Residues: 1-118 <SHL>
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotrimer; immunoglobulin
 F:1-30/Region: framework 1
 F:15-98/Domain: immunoglobulin homology <IMM>
 F:31-35/Region: complementarity-determining 1

F/1-6/Domain: signal sequence (fragment) #status predicted <SIG>
F/7-115/Product: Ig light chain #status predicted <MAT>
F/22-96/Domain: immunoglobulin homology <IMM>
F/30-40/Region: complementarity-determining 1
F/56-62/Region: complementarity-determining 2

Query Match 39.5%; Score 520; DB 2; Length 115;
Best Local Similarity 91.7%; Pred. No. 1.2e-28;
Matches 99; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 DIOMTQTSSLSASLGDRVTSCRASODIRNYLNWYQOKPDGTVKFLIYYTSRLQPGVPS 60
DB 7 DIOMTQTSSLSASLGDRVTSCRASODIRNYLNWYQOKPDGTVKFLIYYTSRLHSGVPS 66
QY 61 RFSGSGSGTDYSLTINMLEQEDIGTYFCQOGNTPMTFGGCTKLEIKR 108
DB 67 RFSGSGSGTDYSLTINMLEQEDIGTYFCQOGNTPMTFGGCTKLEIKR 114

RESULT 11

Ig kappa chain V region - mouse
C/Species: Mus musculus (house mouse)
C/Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000
C/Accession: S38862
R/Fischer, R.; Voss, A.; Hunziker, W.; Stierhof, Y.D.; Kreuzaler, F.
submitted to the EMBL Data Library, August 1993
A/Description: Production and cloning of TMV-specific monoclonal antibodies.
A/Reference number: S37200
A/Accession: S38862
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-108 <PTS>
A/Cross-references: EMBL:X75854; NID:G429109; PID:G429110
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/16-90/Domain: immunoglobulin homology <IMM>

Query Match 39.4%; Score 519.5; DB 2; Length 108;
Best Local Similarity 90.7%; Pred. No. 1.2e-28;
Matches 99; Conservative 4; Mismatches 5; Indels 1; Gaps 1;

QY 1 DIOMTQTSSLSASLGDRVTSCRASODIRNYLNWYQOKPDGTVKFLIYYTSRLQPGVPS 60
DB 1 DIOMTQTSSLSASLGDRVTSCRASODIRNYLNWYQOKPDGTVKFLIYYTSRLHSGVPS 60
QY 61 RFSGSGSGTDYSLTINMLEQEDIGTYFCQOGNTPMTFGGCTKLEIKR 107
DB 61 RFSGSGSGTDYSLTINMLEQEDIGTYFCQOGNTPMTFGGCTKLEIKR 108

RESULT 12

Ig kappa chain precursor V region (5-27) - mouse
C/Species: Mus musculus (house mouse)
C/Date: 27-Jul-1990 #sequence_revision 27-Jul-1990 #text_change 21-Jan-2000
C/Accession: A34904
R/Bedzyk, W.D.; Herron, J.N.; Edmundson, A.B.; Voss Jr., E.W.
J. Biol. Chem. 265, 133-138, 1990
A/Title: Active site structure and antigen binding properties of idiotypically cross-reactive antibodies: heterotetramer; immunoglobulin
A/Reference number: A34903; MUID:90094387; PMID:2104617
A/Accession: A34904
A/Status: preliminary; not compared with conceptual translation
A/Molecule type: mRNA
A/Residues: 1-126 <BED>
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/35-109/Domain: immunoglobulin homology <IMM>

Query Match 39.3%; Score 518; DB 2; Length 126;
Best Local Similarity 92.5%; Pred. No. 1.7e-28;
Matches 98; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 DIOMTQTSSLSASLGDRVTSCRASODIRNYLNWYQOKPDGTVKFLIYYTSRLQPGVPS 60
DB 20 DIOMTQTSSLSASLGDRVTSCRASODIRNYLNWYQOKPDGTVKFLIYYTSRLHSGVPS 79
QY 61 RFSGSGSGTDYSLTINMLEQEDIGTYFCQOGNTPMTFGGCTKLEIKR 106
DB 80 RFSGSGSGTDYSLTINMLEQEDIGTYFCQOGNTPMTFGGCTKLEIKR 125

RESULT 13

Ig heavy chain V region (anti-DNA, 3H9VH) - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 16-Aug-1996
C/Accession: P10234
R/Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Plesetsky, D.; Marshak-Rothstein, A.
J. Exp. Med. 171, 265-297, 1990
A/Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic hypermutation
A/Reference number: P10231; MUID:9011618; PMID:2104919
A/Accession: P10234
A/Molecule type: mRNA
A/Residues: 1-117 <SHL>
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/1-30/Region: framework 1
F/15-98/Domain: immunoglobulin homology <IMM>
F/31-35/Region: complementarity-determining 1
F/36-49/Region: framework 2
F/50-66/Region: complementarity-determining 2
F/67-98/Region: framework 3
F/99-109/Region: complementarity-determining 3
F/110-117/Region: framework 4

Query Match 39.1%; Score 515.5; DB 2; Length 117;
Best Local Similarity 84.6%; Pred. No. 2.4e-28;
Matches 99; Conservative 5; Mismatches 12; Indels 1; Gaps 1;

QY 129 EVOLQSGPELVKGAAGVKSCKDGYAFNSMWNWYQOKPDGTVKFLIYYTSRLQPGVPS 188
DB 1 QVQIQSGPELVKGAAGVKSCKDGYAFNSMWNWYQOKPDGTVKFLIYYTSRLQPGVPS 60
QY 189 NGKFEGRKILTAQSSSTAYVQLSSTVDSAYVFCARS-GLRIYANDYGGGTSVT 244
DB 61 NGKFEGRKILTAQSSSTAYVQLSSTVDSAYVFCARS-GLRIYANDYGGGTSVT 117

RESULT 14

Ig kappa chain (clone KL2.21) - mouse
C/Species: Mus musculus (house mouse)
C/Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 21-Jan-2000
C/Accession: S69901
R/Wysocki, L.J.; Creighton, G.; Lehmann, K.R.; Cambier, J.C.
Immunology 75, 116-121, 1992
A/Title: B-cell proliferation initiated by Ia cross-linking and sustained by interleukin 4
A/Reference number: S69900; MUID:92165291; PMID:1537587
A/Accession: S69901
A/Status: preliminary; translation not shown
A/Molecule type: DNA
A/Residues: 1-107 <WYS>
A/Cross-references: EMBL:X55042; NID:G511025; PID:CAA38882.1; PID:G511026
C/Superfamily: immunoglobulin V region; immunoglobulin homology
F/16-90/Domain: immunoglobulin homology <IMM>

Query Match 38.8%; Score 511.5; DB 2; Length 107;
Best Local Similarity 91.7%; Pred. No. 4e-28;
Matches 99; Conservative 2; Mismatches 6; Indels 1; Gaps 1;

QY 1 DIOMTQTSSLSASLGDRVTSCRASODIRNYLNWYQOKPDGTVKFLIYYTSRLQPGVPS 60
DB 1 DIOMTQTSSLSASLGDRVTSCRASODIRNYLNWYQOKPDGTVKFLIYYTSRLHSGVPS 60
QY 61 RFSGSGSGTDYSLTINMLEQEDIGTYFCQOGNTPMTFGGCTKLEIKR 108

Db 61 RFSGSGSGTDYSLTISNLEQEDIALYFCQOGNT-LMTFGGTYLTIKR 107

RESULT 15

KWSAR

Ig kappa chain V regions (anti-arsenate hybridoma proteins) - mouse

C/Species: Mus musculus (house mouse)

C/Date: 06-Jul-1982 #sequence_revision 06-Jul-1982 #text_change 21-Jan-2000

C/Accession: A01927

R/Siegelman, M.; Capra, J.D.

Proc. Natl. Acad. Sci. U.S.A. 78, 7679-7683, 1981

A/Title: Complete amino acid sequence of light chain variable regions derived from five

A/Reference number: A01927; MID:82150934; PMID:6801658

A/Accession: A01927

A/Molecule type: protein

A/Residues: 1-108 <SIB>

A/Experimental source: strain A/J

A/Note: hp 93G7 differs in having 93-Met; HP 123E6 differs in having 7-Ser, 92-Tyr, and

Arg, 84-Ser, and 93-Ala

C/Comment: The sequence shown is HP R16.7.

C/Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa)

chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 1A

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer

F/16-90/Domain: immunoglobulin homology <IMM>

F/23-88/Disulfide bonds: #status predicted

Query Match 38.8%; Score 511; DB 1; Length 108;
Best Local Similarity 90.7%; Pred. No. 4.4e-28;
Matches 98; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY	1	DIOMTOTSLSASLSDRVVSCRASQDIRNYLMTYQKPKDGVKFLIYYTSRLQGVPS	60
Db	1	DIOMTOTSLSASLSDRVVSCRASQDIRNYLMTYQKPKDGVKFLIYYTSRLQGVPS	60
QY	61	RFSGSGSGTDYSLTINNLEQEDIGTYFCQOGNTPTPTFGGTYLTIKR	108
Db	61	RFSGSGSGTDYSLTINNLEQEDIGTYFCQOGNTPTPTFGGTYLTIKR	108

Search completed: April 22, 2004, 11:57:11
Job time: 14 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 22, 2004, 11:45:27 ; Search time 51 Seconds
(without alignments)

1368.416 Million cell updates/sec

Title: US-10-620-049-23

Perfect score: 1317

Sequence: 1 DIQWTQYTSLSASLGRVT.....GLRYPADYWGQGRSVTVSS 247

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1250	94.9	247	6	AAO27253
2	1249	94.8	247	6	AAO27253
3	1242	94.3	247	6	AAO27252
4	1240	94.2	247	6	AAO27254
5	1237	93.9	247	6	AAO27256
6	994	75.5	637	5	AAU75365
7	994	75.5	637	5	AAU75370
8	994	75.5	656	5	AAU75383
9	994	75.5	657	5	AAU75389
10	992	75.3	601	3	AAO27461
11	992	75.3	601	3	ABG72265
12	992	75.3	642	5	AAU75382
13	992	75.3	642	5	AAO29675
14	992	75.3	643	5	AAU75390
15	992	75.3	643	5	AAO29670
16	988.5	75.1	895	5	AAU75369
17	988.5	75.1	895	5	AAU75368
18	988.5	75.1	895	5	AAU75374
19	988.5	75.1	895	5	AAO29673
20	988.5	75.1	896	5	AAU75367
21	988.5	75.1	896	5	AAU75366
22	988.5	75.1	896	5	AAU75373
23	988.5	75.1	896	5	AAO29672
24	988.5	75.1	896	6	AAO29671
25	988.5	75.1	896	6	AAO29676

26	988.5	75.1	899	5	AAU75375	AAU75375	Diphtheri
27	988.5	75.1	899	5	AAO29674	AAO29674	Anti-T ce
28	984.5	74.8	652	5	AAU75448	AAU75448	Immunotox
29	954	72.4	302	2	AAO60206	AAO60206	Bispecific
30	953.5	72.4	554	3	AAU50822	AAU50822	Fv-antibo
31	948	72.0	504	7	ADD25787	ADD25787	Binding d
32	948	72.0	555	7	AD866039	AD866039	Anti-CD3
33	924	70.2	562	6	ABR57058	ABR57058	Plasmiid p
34	920.5	69.9	531	3	AAU43749	AAU43749	Amino aci
35	911	69.2	271	5	ABG31022	ABG31022	Mouse sin
36	911	69.2	271	7	ADD25451	ADD25451	Binding d
37	895	68.0	251	4	AAU74793	AAU74793	Single ch
38	895	68.0	258	4	AAU74794	AAU74794	Single ch
39	888	67.4	543	7	ADD12876	ADD12876	CD28/mela
40	881	66.9	507	5	AAU72858	AAU72858	BG7C10x4-
41	868	65.9	539	3	AAU50823	AAU50823	Fv-antibo
42	865	65.8	562	6	ABR57059	ABR57059	Plasmiid p
43	851.5	64.7	436	3	AAU91036	AAU91036	Apoptobod
44	848	64.4	650	6	ABR62591	ABR62591	Anti-CD7
45	848	64.4	651	6	ABR62590	ABR62590	Anti-CD7

ALIGNMENTS

RESULT 1	AAO27253	standard; protein; 247 AA.
ID	AAO27253	
XX	AAO27253	
AC	AAO27253	
XX	17-SEP-2003	(first entry)
DE	Antibody 14B7 scFv mutant A2E amino acid sequence.	
XX	Mouse; murine; affinity-matured recombinant antibody;	
KX	proteinaceous toxin; Bacillus anthracis protective antigen;	
KM	antibacterial; gene therapy; vaccine; biological warfare agent;	
XX	infection; hybridoma; scFv; 14B7; mutant; mutein; A2E.	
XX	Misc SP.	
OS	Synthetic.	
XX		
FT	Key	Location/Qualifiers
FT	Region	1..108
FT	Region	/label= Light_chain
FT	Region	1..23
FT	Region	/label= LFR1
FT	Region	/note= "Light chain framework region 1"
FT	Region	24..34
FT	Region	/label= CDR L1
FT	Region	/note= "Complementarity determining region L1"
FT	Region	35..49
FT	Region	/label= LFR2
FT	Region	/note= "Light chain framework region 2"
FT	Region	50..56
FT	Region	/label= CDR L2
FT	Region	/note= "Complementarity determining region L2"
FT	Misc-difference	56
FT	Region	/note= "Wild-type Ser substituted by Pro"
FT	Region	57..88
FT	Region	/label= LFR3
FT	Region	/note= "Light chain framework region 3"
FT	Region	89..97
FT	Region	/label= CDR L3
FT	Region	/note= "Complementarity determining region L3"
FT	Region	98..108
FT	Region	/label= LFR4
FT	Region	/note= "Light chain framework region 4"
FT	Region	109..128
FT	Region	/label= Linker
FT	Region	/note= "(GlySer)4 linker"
FT	Region	129..247

FT		/label= Heavy_chain
FT	Region	129..154
FT		/label= HFR1
FT		/note= "Heavy chain framework region 1"
FT	Region	155..163
FT		/label= CDR_H1
FT		/note= "Complementarity determining region H1"
FT	Region	164..177
FT		/label= HFR2
FT		/note= "Heavy chain framework region 2"
FT	Region	178..194
FT		/label= CDR_H2
FT		/note= "Complementarity determining region H2"
FT	Region	195..226
FT		/label= HFR3
FT		/note= "Heavy chain framework region 3"
FT	Region	227..236
FT		/label= CDR_H3
FT		/note= "Complementarity determining region H3"
FT	Region	237..247
FT		/label= HFR4
FT		/note= "Heavy chain framework region 4"
PX		WO2003040384-A1.
PN		
PD		15-MAY-2003.
PF		05-NOV-2002; 2002WO-US035567.
PR		05-NOV-2001; 2001US-0332849P.
PA		(TEXA) UNIV TEXAS SYSTEM.
PI		Georgiou G, Iverson BL, Maynard JA;
DK		WPI; 2003-430672/40.
XX		
PT		New purified affinity-matured recombinant antibody with binding specificity for Bacillus anthracis protective antigen, useful for diagnosing, preventing or treating anthrax or other bacterial infections.
PS		Example; Page; 48pp; English.
CC		This invention relates a purified affinity-matured recombinant antibody or its portion having binding specificity for a proteinaceous toxin or a Bacillus anthracis protective antigen. The antibody may have an antibacterial activity and may be used in gene therapy or a vaccine.
CC		Bacillus anthracis, commonly referred to as was one of the first biological warfare agents to be developed and is now perceived as a major threat worldwide. The composition and methods of the invention may be useful in diagnosing, preventing or treating infections caused by Bacillus anthracis and other bacterial toxins. The present sequence is that of the mouse wild-type anti-protective antigen hyridoma antibody 1A8T serV mutant A2E, with a synthetic linker (Gly4Ser)4 between the light and heavy chains. This antibody had a Ser56Pro substitution compared to the wild-type sequence (see AA027252) and was developed in the examples of the specification in order to identify antibodies which had increased binding affinity for the bacillus anthracis toxin. Note: This sequence does not appear in the specification but was created by the indexer using information given in the examples and figure 4 of the disclosure
SQ		Sequence 247 AA;
Query Match	94.9%; Score 1250; DB 6; Length 247;	
Best Local Similarity	95.1%; Pred. No. 1.8e-76;	
Matches 235; Conservative	5; Mismatches 7; Indels 0; Gaps 0;	
QY	1 DIQMGTSSLSASIGDPRTVSCSPDIRNLTNNYQQCPDQTKAFIYYTSRLPGVPS 60 1 :: :: :: :: :: :: :: :: :: 1 DIQM:QTSSLSASIGDRVTISCRASQDIRNLNTNNYQQCPDQTVKLIIYTSRLPGVPS 60	

Db	61	REGSSSSGTDYSLTSLTNSQEDIGYFPGQGNILPMFFGGTUKLEIRGGGGSGGGSSG	120
Qy	121	GGSGGGGGSFVQLQSGSPFLVYKPGASVKISCDSGIAFNSSMMWVKRPGQGLEMERIT	180
Db	121	GGSGGGGGSFVQLQSGSPFLVYKPGASVKISCDSGIAFNSSMMWVKRPGQGLEWIGRIT	180
Qy	181	PGDGSNNYKGEKGAIIITADKSSSETAYMQSLSTVDSAVYFCARSGLLRYANDYQGQ	240
Db	181	PGDGDINNYKGEKGRNITITADKSSSETAYMQSLSTVDSAVYFCARSGLLRYANDYQGQ	240
Qy	241	TSYTVSS 247	
Db	241	TSYTVSS 247	

ID	AAO27255	standard; protein; 247 AA.
XX	AAO27255;	
DT	17-SEP-2003	(first entry)
XX	Antibody 14B7 scFv mutant 6A amino acid sequence.	
DE		
XX	Mouse; murine; affinity-matured recombinant antibody;	
KW	proteinaceous toxin; Bacillus anthracis protective antigen;	
KW	antibacterial; gene therapy; vaccinia; biological warfare agent	
KX	infection; hybridoma; scFv; 14B7; mutant; mutein; 6A.	
XX		
OS	Mus sp.	
OS	Synthetic.	
PH	Key	Location/Qualifiers
FT	Region	1..108
FT		/label= Light_chain
FT	Region	1..23
FT		/label= LFR1
FT		/note= "Light chain framework region 1"
FT	Region	24..34
FT		/label= CDR L1
FT		/note= "Complementarity determining region L1"
FT	Region	35..49
FT		/label= LFR2
FT		/note= "Light chain framework region 2"
FT	Misc-difference	46
FT		/note= "Wild-type Leu substituted by Phe"
FT	Region	50..56
FT		/label= CDR L2
FT		/note= "Complementarity determining region L2"
FT	Misc-difference	56
FT		/note= "Wild-type Ser substituted by Pro"
FT	Region	57..88
FT		/label= LFR3
FT		/note= "Light chain framework region 3"
FT	Region	89..97
FT		/label= CDR L3
FT		/note= "Complementarity determining region L3"
FT	Region	98..108
FT		/label= LFR4
FT		/note= "Light chain framework region 4"
FT	Region	109..128
FT		/label= Linker
FT		/note= "(Gly4Ser)4 linker"
FT	Misc-difference	118
FT		/note= "Wild-type Ser substituted by Thr"
FT	Region	129..247
FT		/label= Heavy_chain
FT	Region	129..154
FT		/label= HFR1

FT FT /label= CDR H1
FT FT /note= "Complementarity determining region H1"
FT FT 164..177
FT FT /label= HFR2
FT FT /note= "Heavy chain framework region 2"
FT Region
FT FT 178..194
FT FT /label= CDR H2
FT FT /note= "Complementarity determining region H2"
FT Region
FT FT 195..226
FT FT /label= HFR3
FT FT /note= "Heavy chain framework region 3"
FT Misc-difference
FT FT 207
FT FT /note= "Wild-type Ala substituted by Glu"
FT Region
FT FT 227..236
FT FT /label= CDR H3
FT FT /note= "Complementarity determining region H3"
FT Region
FT FT 237..247
FT FT /label= HFR4
FT FT /note= "Heavy chain framework region 4"
XX WO2003040384-A1.
XX PN
XX XX
XX PD 15-MAY-2003.
XX XX
XX PP 05-NOV-2002; 2002WO-US035567.
XX XX
XX PR 05-NOV-2001; 2001US-0332849P.
XX XX
XX PA (TEXA) UNIV TEXAS SYSTEM.
XX XX
XX PI Georgiou G, Iverson BL, Maynard JA;
XX DR WPI, 2003-430672/40.
XX XX
XX PT New purified affinity-matured recombinant antibody with binding
XX PT specificity for Bacillus anthracis protective antigen, useful for
XX PT diagnosing, preventing or treating anthrax or other bacterial infections.
XX PS
XX PS Example; Page: 48pp; English.

This invention relates a purified affinity-matured recombinant antibody or its portion having binding specificity for a proteinaceous toxin or a Bacillus anthracis protective antigen. The antibody may have an antibacterial activity and may be used in gene therapy or a vaccine. Bacillus anthracis, commonly referred to as was one of the first biological warfare agents to be developed and is now perceived as a major threat worldwide. The composition and methods of the invention may be useful in diagnosing, preventing or treating infections caused by Bacillus anthracis and other bacterial toxins. The present sequence is that of the mouse wild-type anti-protective antigen hybridoma antibody 14B7 scFv mutant 6A, with a synthetic linker (Gly4Ser)4 between the light and heavy chains. This antibody had Leu46Phe, Ser56Pro, Ser118Thr and Ala207Val substitutions compared to the wild-type sequence (see A02752) and was developed in the examples of the specification in order to identify antibodies which had increased binding affinity for the Bacillus anthracis toxin. Note: This sequence does not appear in the specification but was created by the indexer using information given in the examples and Figure 4 of the disclosure

```

Query Match      94.8%  Score 1249; DB 6; Length 247;
Best Local Similarity 94.7%  Pred. No. 2,1e-76;
Matches 234; Conservative 6; Mismatches 7; Indels 0; Gaps 0

```

QY 1 DIQMTQTLLSASLIGRVTASCRASQDIIRNTYINWQKRPDVTFFLLYYTSRLQPGVPS 60

Db 1 DIQMTQTLLSASLIGRVTISCRASQDIIRNTYINWQKRPDVTFFLLYYTSRLQPGVPS 60

QY 61 RPSGSGSTDYSLTINLLEQEDIGTFYCCQGNRPPTFGGGRKLEIKRGGGSGDGGGCG 120

Db 61 RPSGSGSTDYSLTINLLEQEDIGTFYCCQGNLPTPTFGGGRKLEIKRGGGSGGCGGCG 120

Qy	12	GGGGGGGGSVQLOOQSGPELVEYFGASVVKISCDQSGAFNFSMMNNWVKRPPGGGJEMIRIY	180
Db	121	GGGGGGGGSVQLOOQSGPELVEYFGASVVKISCDQSGAFNFSMMNNWVKRPPGGGJEMIRIY	180
Qy	181	PGGGSDNNYNGKEGKRAITLADKSSSTAYWQSLSTVDSAYYFCARSGLLRYANDYWGQG	240
Db	181	PGGGSDNNYNGKEGKRAITLADKSSSTAYWQSLSTVDSAYYFCARSGLLRYANDYWGQG	240
Qy	241	TSVTSS 247	
Db	241	TSVTSS 247	

RESULT 3
AAO27252
ID AAO27252 standard; protein; 247 AA

AC AA027252;

DT 17-SEP-2003 (first entry)

DE Antibody 14B7 scFv wild type amino acid sequence

KW Mouse; murine; affinity-matured recombinant antibody; anti-*Salmonella* typhimurium; protective; neutralizing

antibacterial; gene therapy; vaccine; biological warfare agent;

2000

05 Synthetic.
yy

FH	Key	Location/Qualifiers
ET	Section	1 108

Region	Label= Light_chain
1	23

```
FT /label= LfRI
FT /note= "light chain framework region 1"
```

Region	24. :34	CDR L1
ET		
ET		

Region	/notes "completeness" determining reg
PT	35. .49

```

E1 /label= UFR2
FT /note= "Light chain framework region 2"

```

FT	region	30+.30	/label=	CDR	I2
----	--------	--------	---------	-----	----

Region	FT
57.88	

```

14 /note= "Light chain framework region 3"
15 FT

```

FT	CDR_L3
FT	CDR_L3

Region	98. .108
FT	

/note= "Light chain framework region 4

```

/label= linker

```

Region	129.	.247
FT		

FT	Region	129.154
FT		

FT	Region	/note= "Heavy chain framework region 1
FT	155	163

```
ET      /label= CDR_H1
ET      /note= "Complementarity determining region H1"
```

FT	Region	164.177
FT	/label= HFR2	.

Region	/NOTES="Heavy chain framework region 2
FT	178. .194

```

FT      /label= CDR_H2
FT      /note= "Complementarity determining region H2"

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FI	Region	1991	1992
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FT FT /label= HPR3
FT FT /note= "Heavy chain framework region 3"
FT FT 227. .236
FT FT /label= CDR_H3
FT FT /note= "Complementarity determining region H3"
FT FT 237. .247
FT FT /label= HPR4
FT FT /note= "Heavy chain framework region 4"
XX XX
XX XX W02003040384-A1.
XX PD 15-MAY-2003.
XX XX
XX XX 05-NOV-2002; 2002MO-US035567.
XX XX
XX XX 05-NOV-2001; 2001US-0332849P.
XX XX
XX XX (TEXA ) UNIV TEXAS SYSTEM.
XX XX
XX XX Georgiou G, Iverson BL, Maynard JA;
XX XX WPI, 2003-430672/40.
XX XX
XX XX New purified affinity-matured recombinant antibody with binding
XX XX specificity for Bacillus anthracis protective antigen, useful for
XX XX diagnosing, preventing or treating anthrax or other bacterial infections.
XX XX
XX XX Example; Fig 4; 48pp; English.
XX XX
XX XX This invention relates a purified affinity-matured recombinant antibody
XX XX or its portion having binding specificity for a proteinaceous toxin or a
XX XX Bacillus anthracis protective antigen. The antibody may have an
XX XX antibacterial activity and may be used in gene therapy or a vaccine.
XX XX Bacillus anthracis, commonly referred to as was one of the first
XX XX biological warfare agents to be developed and is now perceived as a major
XX XX threat worldwide. The composition and methods of the invention may be
XX XX useful in diagnosing, preventing or treating infections caused by
XX XX Bacillus anthracis and other bacterial toxins. The present sequence is
XX XX that of the mouse wild-type anti-protective antigen hybridoma antibody
XX XX 14B7 scFv, with a synthetic linker (GlySer)4 between the light and heavy
XX XX chains. This antibody was used for the development of mutant antibodies
XX XX (see AAO27253-6) which had increased binding affinity for the Bacillus
XX XX anthracis toxin in the examples of the specification
XX XX
XX XX Sequence 247 AA:
XX
XX Query Match 94.3%; Score 1242; DB 6; Length 247;
XX Best Local Similarity 94.7%; Pred. No. 6.1e-76;
XX Matches 234; Conservative 5; Mismatches 8; Indels 0; Gaps 0;
XX
XX 1 DIOMTQTSSASISGDEVTSCRASODIRNYLMWYOOKPDGTGKFLIYTSRLOPVPVS 60
XX 1 DIONTQTSSASISGDEVTSCRASODIRNYLMWYOOKPDGTGKFLIYTSRLOPVPVS 60
XX 1 DIONTQTSSASISGDEVTSCRASODIRNYLMWYOOKPDGTGKFLIYTSRLOPVPVS 60
XX 61 RFSGSGSGTDYSLTINLEDEDIGTFYFCQGNTPPTWPGGTGKLEIRGGGSDGSGSGG 120
XX 61 RFSGSGSGTDYSLTINLEDEDIGTFYFCQGNTPPTWPGGTGKLEIRGGGSDGSGSGG 120
XX 61 RFSGSGSGTDYSLTINLEDEDIGTFYFCQGNTPPTWPGGTGKLEIRGGGSDGSGSGG 120
XX 61 RFSGSGSGTDYSLTINLEDEDIGTFYFCQGNTPPTWPGGTGKLEIRGGGSDGSGSGG 120
XX 121 GSGSGSGSEVQLQDSGPELVKPGASVKISKDSDGYAFSSMMNWVKORPGQGLEWIGRIY 180
XX 121 GSGSGSGSEVQLQDSGPELVKPGASVKISKDSDGYAFSSMMNWVKORPGQGLEWIGRIY 180
XX 121 GSGSGSGSEVQLQDSGPELVKPGASVKISKDSDGYAFSSMMNWVKORPGQGLEWIGRIY 180
XX 181 PGDGDSTNNGKFEKALITADKSSSTAYWQLSLTSDSAVYFCARSGLLRYANDYWGQG 240
XX 181 PGDGDSTNNGKFEKALITADKSSSTAYWQLSLTSDSAVYFCARSGLLRYANDYWGQG 240
XX 181 PGDGDSTNNGKFEKALITADKSSSTAYWQLSLTSDSAVYFCARSGLLRYANDYWGQG 240
XX 241 TSVTYSS 247
XX 241 TSVTYSS 247
XX 241 TSVTYSS 247
XX
XX RESULT 4
XX AAO27254

```

```

ID AAO27254 standard; protein; 247 AA.
XX XX
XX XX AAO27254;
AC AC
XX XX 17-SEP-2003 (first entry)
XX XX
XX XX
XX XX Antibody 14B7 scFv mutant 1H amino acid sequence.
XX XX
XX XX Mouse; murine; affinity-matured recombinant antibody;
XX XX proteinaceous toxin; Bacillus anthracis protective antigen;
XX XX antibacterial; gene therapy; vaccine; biological warfare agent;
XX XX infection; hybridoma; scFv; 14B7; mutant; mutein; 1H.
XX XX
XX XX Mus sp.
XX XX Synthetic.
OS OS
XX XX
XX XX Location/Qualifiers
XX XX 1.108
XX XX /label= Light_chain
XX XX 1.23
XX XX /label= LPR1
XX XX /note= "Light chain framework region 1"
XX XX 24.34
XX XX /label= CDR_L1
XX XX /note= "Complementarity determining region L1"
XX XX 35.49
XX XX /label= LPR2
XX XX /note= "Light chain framework region 2"
XX XX 50.56
XX XX /label= CDR_L2
XX XX /note= "Complementarity determining region L2"
XX XX 55
XX XX /note= "Wild-type Gln substituted by Leu"
XX XX /note= "Wild-type Ser substituted by Pro"
XX XX 57.88
XX XX /label= LPR3
XX XX /note= "Light chain framework region 3"
XX XX 69.97
XX XX /label= CDR_L3
XX XX /note= "Complementarity determining region L3"
XX XX 98.108
XX XX /label= LPR4
XX XX /note= "Light chain framework region 4"
XX XX 107
XX XX /note= "Wild-type Lys substituted by Arg"
XX XX 109.128
XX XX /label= Linker
XX XX /note= "(GlySer)4 linker"
XX XX 129.247
XX XX /label= Heavy_chain
XX XX 129.154
XX XX /label= HPR1
XX XX /note= "Heavy chain framework region 1"
XX XX 155.163
XX XX /label= CDR_H1
XX XX /note= "Complementarity determining region H1"
XX XX 164.177
XX XX /label= HPR2
XX XX /note= "Heavy chain framework region 2"
XX XX 178.194
XX XX /label= CDR_H2
XX XX /note= "Complementarity determining region H2"
XX XX 195.226
XX XX /label= HPR3
XX XX /note= "Heavy chain framework region 3"
XX XX 227.236
XX XX /label= CDR_H3
XX XX /note= "Complementarity determining region H3"
XX XX 237.247
XX XX /label= HPR4
XX XX /note= "Heavy chain framework region 4"
XX XX

```


Thu Apr 22 14:51:00 2004

us-10-620-049-23.rag

Page 6

XX Georgian G, Iverson BL, Maynard JA;
 XX
 XX
 DR WPI, 2003-430672/40.
 XX
 XX New purified affinity-matured recombinant antibody with binding
 PT specificity for *Bacillus anthracis* protective antigen, useful for
 PT diagnosing, preventing or treating anthrax or other bacterial infections
 XS
 XS Example; Page, 48pp; English.

CC This invention relates a purified affinity-matured recombinant antibody
CC or its portion having binding specificity for a proteinaceous toxin or a
CC Bacillus anthracis protective antigen. The antibody may have an
CC antibacterial activity and may be used in gene therapy or a vaccine.
CC Bacillus anthracis, commonly referred to as was one of the first
CC biological warfare agents to be developed and is now perceived as a major
CC threat worldwide. The composition and methods of the invention may be
CC useful in diagnosing, preventing or treating infections caused by
CC Bacillus anthracis and other bacterial toxins. The present sequence is
CC that of the mouse wild-type anti-protective antigen hybridoma antibody
CC 14B7 scfv mutant 197, with a synthetic linker (GlySer)⁴ between the
CC light and heavy chains. This antibody had a Leu225Ia substitution
CC compared to the wild-type sequence (see AAO27225) and was developed in
CC the examples of the specification in order to identify antibodies which
CC had increased binding affinity for the Bacillus anthracis toxin. Note:
CC This sequence does not appear in the specification but was created by the
CC indexer using information given in the examples and Figure 4 of the
CC disclosure

Query Match	93.9%	Score 1237	DB 6	Length 247
Best Local Similarity	94.3%	Pred. No. 1.3e-75		
Matches 233	Conservative	5	Mismatches 9	Indels 0
			Gaps	0

Qy	1	DIQWQTOTSSLSASLGRVAVS	CRAODIRNYINWQCKRPDGTVELLYYSRLQPVGS	60
Db	1	DIQW1QRTSSLSASLGRVAVS	CRAODIRNYINWQCKRPDGTVELLYYSRLQSPGS	60
Qy	61	RFSGSGSGTGYSLTINL	BEODIGTYFCQCGNPMTFGGTXLEIKKGGSGSDGSGSG	120
Db	61	RFSGSGSGTGYSLTINQ	BEODIGTYFCQCGNLTPTFGGTXLEIKKGGSGSGSGSG	120
Qy	121	GGSGSGSGSEVLOOQSGELV	KPGASVKISCKDGYFNSMMNWKKRPGGLWETIGTY	180
Db	121	GGSGSGSGSEVLOOQSGELV	KPGASVKISCKDGYFSSMMNWKKRPGGLWETIGTY	180
Qy	181	PGGDDSNINNGKFEKCAL	LTLDKSSSTAINMQLSLTISVDNAVYFCARSGILIRANDYWGQ	240
Db	181	PGGDDSNINNGEKKALL	TDKSSSTAINMQLSLTISVDNAVYFCARSGILIRANDYWGQ	240
Qy	241	TSVTVSS	247	
Db	241	TSVTVSS	247	

XX	RESULT 6
XX	AAU75365
ID	AAU75365 standard; protein; 637 AA.
XX	
AC	AAU75365;
XX	
DT	23-APR-2002 (first entry)
XX	
DE	Diphtheria toxin/UCHT1 immunotoxin fusion protein #1.
XX	
KW	Immunotoxin; pseudomonas exotoxin A; ERA; diphtheria toxin; DT;
KW	cyclosteric; immunosuppressive; immunostimulant; antidiabetic;
KW	antirheumatic; antituberclic; anti-HIV; anti-inflammatory;
KW	anti-T cell immunotoxin fusion protein; antibody; UCHT1;
KW	T cell leukaemia; lymphoma; graft-versus-host disease; Fv;
KW	autoimmune disease; transplant rejection; systemic lupus erythematosus;

KW	type I diabetes; rheumatoid arthritis; myasthenia gravis;
KW	multiple sclerosis; AIDS; acquired immunodeficiency syndrome;
KM	chronic immunosuppression; (GlySer)3 linker.
XX	
OS	Mus sp.
OS	<i>Corynebacterium diphtheriae</i> .
OS	Synthetic.
OS	Chimeric.
XX	
FN	WC200187982-A2.

FD 22-NOV-2001 .
XX
PE 18-MAY-2001; 2001WO-US016125 .
XX
PR 18-MAY-2000; 2000US-00573797 .
XX
PA (NOVS) NOVARTIS AG.
PA (NOVS) NOVARTIS-ERINDUNGEN VERN GES MBH.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Neville DW, Thompson JT, Hu H, Woo J, Ma S, Hexham JM, Digan ME;
XX
DR WPI; 2002-121980/16 .
XX
XX New anti-T cell immunotoxin fusion protein comprising a truncated
PT diphtheria toxin moiety, a connector, and one single chain Fv of the
PT variable region of a UCHL1 antibody, useful for treating e.g. autoimmune
PT diseases .
XX
PS Claim 17; Page 259-261; 307pp; English.

The invention relates to an anti-T-cell immunotoxin fusion protein, comprising from the amino terminus, a truncated diphtheria toxin moiety, a connector, and one single chain Fv of the variable region of a UCHL1 antibody. The single chain Fv comprises VL, L, or VH. L is a Gly-Ser linker, and VL and VH are the variable light and heavy domains of the anti-CD3 antibody UCHL1. Also included are a nucleic acid encoding the novel immunotoxin fusion protein, a vector comprising the nucleic acid and a cell comprising the nucleic acid. The immunotoxin may also be a pseudomonas endotoxin A (ETA). The immunotoxins are useful for treating T cell leukemias or lymphomas, graft-versus-host diseases, and autoimmune diseases by inducing immune tolerance. The immunotoxin fusion proteins may be used in vivo to systematically reduce populations of T cells, or ex vivo to effect T-cell depletion from a treated cell population. The fusion protein can be administered to a subject who is or will be a recipient of an allograft to prevent or reduce T-cell mediated acute or chronic transplant rejection of the transplanted allogeneic cells, tissue or organ in the subject as well as treat other T-cell mediated diseases such as systemic lupus erythematosus, type I diabetes, rheumatoid arthritis, myasthenia gravis, multiple sclerosis, infectious diseases of the immune system (e.g. AIDS (acquired immunodeficiency syndrome)) and chronic immunosuppression. The present sequence is an immunotoxin fusion protein of the invention comprising 350 residues from the N-terminal glycine of mature DT toxin, a (GlySer)₃ linker and one single Fv chain from antibody UCHL1.

```

SQ      Sequence 637 AA;
Query Match 75.5%; Score 994; DB 5; Length 637;
Beet Local Similarity 78.0%; Pred. No. 7.1e-59;
Matches 195; Conservative 13; Mismatches 34; Indels 8; Gaps 2.

QY      1 DIQMOTTSSASISGDRVTWSCASQDIRNYLWYQKQKPDGYKFLIYTSRLQPVPS 60
Db      393 DIQMOTTSSASISGDRVTWSCASQDIRNYLWYQKQKPDGYKFLIYTSRLHSQVPS 452

QY      61 RPSGSGSTDVSLTNNLEQEDIGYFQOQNTPTPWTGGGTGTXLEIKRGGGSGSOGGSGG 120
Db      453 RPSGSGSTDVSLTNNLEQEDIGYFQOQNTLPTWTFAGTKLEIKRGGGSGG 507

QY      121 GSGSGSGSEVQLQOQGPFLVYKPGASVKISCKDQSGVAFNPSMMNWVKKRPPQGLEWIGRIY 180

```


XX WPI; 2002-121980/16.
XX
XX New anti-T cell immunotoxin fusion protein comprising a truncated
PT diphtheria toxin moiety, a connector, and one single chain Fv of the
PT variable region of a UCHL1 antibody, useful for treating e.g. autoimmune
PT diseases.
XX
XX Disclosure; Page 282-283; 307pp; English.

XX The invention relates to an anti-T cell immunotoxin fusion protein,
XX comprising from the amino terminus, a truncated diphtheria toxin moiety,
XX a connector, and one single chain Fv of the variable region of a UCHL1
XX antibody. The single chain Fv comprises VL, L, or VH, L is a Gly-Ser
XX linker, and VL and VH are the variable light and heavy domains of the
XX anti-CD3 antibody UCHL1. Also included are a nucleic acid encoding the
XX novel immunotoxin fusion protein, a vector comprising the nucleic acid
XX and a cell comprising the nucleic acid. The immunotoxin may also be a
XX pseudomonas endotoxin A (ETA). The immunotoxins are useful for treating T
XX cell leukemias or lymphomas, graft-versus-host diseases, and autoimmune
XX diseases by inducing immune tolerance. The immunotoxin fusion proteins
XX may be used in vivo to systemically reduce populations of T cells, or ex
XX vivo to effect T-cell depletion from a treated cell population. The
XX fusion proteins can be administered to a subject who is or will be a
XX recipient of an allotransplant to prevent or reduce T-cell mediated acute
XX or chronic transplant rejection of the transplanted allogeneic cells,
XX tissue or organ in the subject as well as treat other T-cell mediated
XX diseases such as systemic lupus erythematosus, type I diabetes,
XX rheumatoid arthritis, myasthenia gravis, multiple sclerosis, infectious
XX diseases of the immune system (e.g. AIDS (acquired immunodeficiency
XX syndrome)) and chronic immunosuppression. The present sequence is a
XX protein sequence included in the sequence listing but not mentioned
XX elsewhere in the specification, associated with the immunotoxin fusion
XX proteins of the invention

XX Sequence 656 AA;

Query Match 75.5%; Score 994; DB 5; Length 656;
Best Local Similarity 78.0%; Pred. No. 7.3e-59;
Matches 195; Conservative 13; Mismatches 34; Indels 8; Gaps 2;

QY 1 DIQMTQTSSLSASLGRVTVSCASQDIRNYLMWYQKPDGTVKFLIYTSRLQGVPS 60
DB 412 DIQMTQTSSLSASLGRVTVSCASQDIRNYLMWYQKPDGTVKFLIYTSRLHSGVPS 471
QY 61 RFGSGSGGTDTYSLTINNLEQEDITGTPCOQGNTPMTFGGTLEIKRGGGSGSG 120
DB 472 KFGSGSGGTDTYSLTINNLEQEDITGTPCOQGNTPMTFGGTLEIKRGGGSGSG 526
QY 121 GSGSGSGSEVQLOQSGELVPGASVATISCKDSGYANSSMMWVKORPGQGFEMGRY 180
DB 527 GSGSGSGSEVQLOQSGELVPGASVATISCKDSGYANSSMMWVKORPGQGFEMGRY 186
QY 181 PGDDSNVNGFEGEKALITADKSSSTAYMQLSTVDSAVYFCARSGLL---RYAMDY 237
DB 587 PYKVSRYNKKFKXKACFTYDKSSSTAYMQLSTVDSAVYFCARSGYGDSDWFDW 646
QY 238 GQGTSTVYSS 247
DB 647 GQGTSTVYSS 656

RESULT 9
AAU75389
ID AAU75389 standard; protein; 657 AA.
AC AAU75389;
XX
XX 23-APR-2002 (first entry)
DT
XX
XX Diphtheria toxin/UCHL1 immunotoxin fusion protein H18D1390-sfv.
XX

KM cytosolic; immunosuppressive; immunostimulant; antidiabetic;
KM antirheumatic; antiarthritic; anti-HIV; anti-inflammatory;
KM anti-T cell immunotoxin fusion protein; antibody; UCHL1;
KM (Gly4Ser)3 linker; T cell leukemia; lymphoma; graft-versus-host disease;
KM Fv; autoimmune disease; transplant rejection;
KM systemic lupus erythematosus; type I diabetes; rheumatoid arthritis;
KM myasthenia gravis; multiple sclerosis; AIDS; H18D1390-sfv;
KM acquired immunodeficiency syndrome; chronic immunosuppression.

XX Mus sp.
OS Corynebacterium diphtheriae.
OS Synthetic.
OS Chimeric.
XX WO200187982-A2.
XX
XX 22-NOV-2001.
XX
XX 18-MAY-2001; 2001WO-US016125.
XX
XX 18-MAY-2000; 2000US-00573797.
XX

XX (NOVS) NOVARTIS AG.
XX (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Neville DM, Thompson JT, Hu H, Moo J, Ma S, Hexham JM, Digan ME;
XX
XX WPI; 2002-121980/16.

XX New anti-T cell immunotoxin fusion protein comprising a truncated
PT diphtheria toxin moiety, a connector, and one single chain Fv of the
PT variable region of a UCHL1 antibody, useful for treating e.g. autoimmune
PT diseases.
XX
XX Example 30; Fig 34; 307pp; English.

XX The invention relates to an anti-T cell immunotoxin fusion protein,
XX comprising from the amino terminus, a truncated diphtheria toxin moiety,
XX a connector, and one single chain Fv of the variable region of a UCHL1
XX antibody. The single chain Fv comprises VL, L, or VH, L is a Gly-Ser
XX linker, and VL and VH are the variable light and heavy domains of the
XX anti-CD3 antibody UCHL1. Also included are a nucleic acid encoding the
XX novel immunotoxin fusion protein, a vector comprising the nucleic acid
XX and a cell comprising the nucleic acid. The immunotoxin may also be a
XX pseudomonas endotoxin A (ETA). The immunotoxins are useful for treating T
XX cell leukemias or lymphomas, graft-versus-host diseases, and autoimmune
XX diseases by inducing immune tolerance. The immunotoxin fusion proteins
XX may be used in vivo to systemically reduce populations of T cells, or ex
XX vivo to effect T-cell depletion from a treated cell population. The
XX fusion proteins can be administered to a subject who is or will be a
XX recipient of an allotransplant to prevent or reduce T-cell mediated acute
XX or chronic transplant rejection of the transplanted allogeneic cells,
XX tissue or organ in the subject as well as treat other T-cell mediated
XX diseases such as systemic lupus erythematosus, type I diabetes,
XX rheumatoid arthritis, myasthenia gravis, multiple sclerosis, infectious
XX diseases of the immune system (e.g. AIDS (acquired immunodeficiency
XX syndrome)) and chronic immunosuppression. The present sequence is an
XX immunotoxin fusion protein of the invention comprising 390 residues from
XX the N-terminal glycine of mature DT toxin, a linker and one single Fv
XX chain from antibody UCHL1, H18D1390-sfv

Query Match 75.5%; Score 994; DB 5; Length 657;
Best Local Similarity 78.0%; Pred. No. 7.3e-59;
Matches 195; Conservative 13; Mismatches 34; Indels 8; Gaps 2;

QY 1 DIQMTQTSSLSASLGRVTVSCASQDIRNYLMWYQKPDGTVKFLIYTSRLQGVPS 60
DB 413 DIQMTQTSSLSASLGRVTVSCASQDIRNYLMWYQKPDGTVKFLIYTSRLHSGVPS 472

Dd		473	KRSGSSGSDYDLSLTISNLEGEEDIALYFFCOQGNLTPMTFAGTKEIRGR-----GGGS6G	527
Qy		121	GGSGGGGSEVOLQGSGPELVKPGASVKISCDSGYAFNSSMMNVKORPCQGLEWIGRIY	180
Dd		528	GGSGGGGSEVOLQGSGPELVKPGAMKISCASGYSEFGYTMNVKSHGXNLWMGLIN	587
Qy		181	PBGDSNNXKKEGRKILLADKSSTAYMQLSITVDASATYFCARSGLL---RYAMDYV	237
Dd		588	PYKGVSTYOKREDFATFTVDKSSSTATMLSLTSBDAVTCAKSGTYGDSDWTFDYV	647
Qy		238	GCGTSYTVSS 247 :	
Dd		648	GCGTTLTVFS 657 :	
RESULT 10				
AAB07461	ID	AAB07461	standard; protein; 601 AA.	
XX		AAB07461;		
XX		20-OCT-2000	(first entry)	
Dt				
De		An immunotoxin comprising a CD3 binding domain and p28.		
Xx		Immunotoxin; CD3-binding domain; Pseudomonas exotoxin A; immune system;		
Kw		sctv(UCHL-1)-P28; T-cell mediated disease; transplant rejection;		
Km		host versus graft disease; graft versus host disease;		
Xk		bone marrow transplant.		
Xx		Synthetic.		
Os		Mus sp.		
Os		Pseudomonas aeruginosa.		
Xx				
FH	Key	Location/Qualifiers		
FT	Region	3..112 "variable region of the light chain"		
FT	Region	128..249 /note= "variable region of the heavy chain"		
PN		WO200041474-A2.		
Xx		20-JUL-2000.		
PD				
PF		13-JAN-2000; 2000MO-EP000245.		
Xx		15-JAN-1999; 99US-00232445.		
PR		25-JAN-1999; 99US-00236968.		
PR		07-OCT-1999; 99US-00414134.		
Xx		(NOVS) NOVARTIS AG.		
PA		(NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.		
XX				
pi		Digan ME, Lake P, Wright RW,		
DR		MPJ, 2000-482739/42.		
N-P8DB; AAA58773.				
PT		Recombinant immunotoxin used for prophylaxis and treatment of T-cell		
medicated diseases e.g. transplantation rejection.				
Claim 3; Page 60-63; 75pp; English.				
The present sequence represents a recombinant immunotoxin comprising a CD3-binding domain and a pseudomonas exotoxin A component. It is designated sctv(UCHL-1)-P28. The immunotoxins of the invention are used for the prophylaxis or treatment of T-cell mediated diseases or conditions of the immune system. They are also used to condition a patient to be transplanted with cells, or a tissue or an organ of a donor and for the prophylaxis and/or treatment of acute or chronic transplantation rejection, host versus graft disease and/or graft versus host disease in a patient to undergo a bone marrow transplant, where the				

CC	CD3-bearing cell population in the patient is depleted and an inoculum
CC	comprising isolated bone marrow and/or stem-cell enriched peripheral
CC	blood cells of the donor treated with immunotoxin is inoculated into the
CC	patient
XX	
SQ	Sequence 601 AA;
	Query Match 75.3%; Score 992; DB 3; Length 601;
	Best local similarity 78.8%; Pred. No. 9.1e-59;
	Matches 197; Conservative 12; Mismatches 35; Indels 6; Gaps 3.
DY	1 DIQTMTTSSLSASIGDRVNTSCASODIRNLTWVQKEDGVKRLTYTSRLPQGPS 60
DY	3 DIQMTCTTSSLSASIGDRVITSCRASODIRNLTWVQKEDGVKRLTYTSRLHSGPS 62
OY	61 RPSGSGSGDVEYLITNNLEDEDITGYECQOGNTPPTFGAGTLERKGGSGSDGGSGG 120
DY	63 KRSGSGSGDYSLTISNLQEDDIATYCCQGNTLPWFAGDTLKEIKRAGGS -GGSGGG 121
OY	121 GSGGGGSGSVQLQSGPELVFPGASVKXISCDSGYAFNSMWNVYKRPQGLIEWTGRTY 180
DY	122 G--SGGSGSEVLQSGPELVKPGASMKXISCASGYSFTGYTMVMVQSHGXLEWNGLIN 179
OY	181 PGDGDNVNYKRFEGALITADKSSTAYMQSLTSVDSAVFPCARSGLL--RYAMDYM 237
DY	180 PYGVISTYQKKDKDALITLDKSSSTAYMELSLTSDSANVTYCAISGYIGSDMYFDWM 239
OY	238 GGGTSYTVSS 247
DY	240 GAGTTVTSS 249
XX	
RESULT 11	
ID	ABG72265 standard; protein; 601 AA.
XX	ABG72265;
AC	ABG72265;
XX	
DL	06-MAR-2003 (first entry)
XX	
DE	Recombinant immunotoxin, scFv/UCHT-1- PE38.
XX	
KW	Recombinant immunotoxin; scFv(UCHT-1)-PE38; single chain Fv fragment;
KW	muring; anti-human CD3-monoclonal antibody binding domain; UCHT-1;
KW	Pseudomonas aeruginosa; exotoxin A; ADP-ribosylating; translocation;
KW	T-cell mediated disorder; organ transplantation rejection;
KW	autoimmune disease; graft versus host disease; bone marrow transplant;
KW	acquired immunodeficiency syndrome; AIDS; T-cell leukaemia;
KW	T-cell lymphoma; T-cell-mediated autoimmune disease; type I diabetes;
KW	systemic lupus erythematosus; rheumatoid arthritis; myasthenia gravis;
KW	multiple sclerosis; immunological tolerance; osteoporosis;
KW	aplastic anaemia; Gaucher's disease; thalassemia; mutant; mutein.
XX	
OS	Mus sp.
OS	Pseudomonas aeruginosa.
OS	Synthetic.
OS	Chimeric.
XX	
FH	Key
FT	Region
	/note= "light chain variable region (VL) "
FT	Peptide
	/note= "linker peptide (L) "
FT	Region
	/note= "heavy chain variable region (VH) "
FT	Peptide
	/note= "connector peptide (C) "
FT	Region
	/note= "PE38 mutant"
US2002142000-A1.	
PD	03-OCT-2002.

XX PF 10-JAN-2000; 2000US-00480236.
 XX PR 10-JAN-2000; 2000US-00480236.
 XX PA (DIGA/) DIGAN M E.
 XX PA (LAKE/) LAKE P.
 XX PA (WRIGHT/) WRIGHT R M.
 XX PI Digan ME, Lake P, Wright RM;
 XX DR MPI; 2003-155935/15.
 XX DR N-PDSB; ABX14413.
 XX PT Novel recombinant immunotoxin polypeptide useful for treatment or
 PT prophylaxis of T-cell mediated disorders or organ transplantation
 PT rejection, comprises a CD3-binding domain and a pseudomonas exotoxin
 PT mutant.
 XX PS Claim 17; Fig 15; 58pp; English.
 XX CC The present invention relates to a novel recombinant immunotoxin,
 CC scFv(UCHT-1)-PE38, and the polynucleotide sequence encoding it. The
 CC recombinant immunotoxin comprising a single chain (sc) Fv fragment of
 CC murine anti-human CD3-monoclonal antibody (UCHT-1) binding domain fused
 CC to a Pseudomonas aeruginosa exotoxin A (PE38) mutant having ADP-
 CC ribosylating and translocation functions but substantially diminished
 CC cell-binding ability. The recombinant immunotoxin is useful for the
 CC treatment or prophylaxis of T-cell mediated disorders, organ
 CC transplantation rejection or autoimmune disease in a patient. For
 CC example, scFv(UCHT-1)-PE38 may be used for treatment or prophylaxis
 CC against graft versus host disease in a patient undergoing a bone marrow
 CC transplant, for the treatment or prophylaxis of transplant rejection in a
 CC patient to undergo a bone marrow transplant, or for conditioning a
 CC patient to be transplanted with cells, tissue or organ of a donor.
 CC scFv(UCHT-1)-PE38 is also useful for treating acquired immunodeficiency
 CC syndrome (AIDS), T-cell leukemias or lymphomas, T-cell-mediated
 CC autoimmune disease such as systemic lupus erythematosus, type I diabetes,
 CC rheumatoid arthritis, myasthenia gravis, multiple sclerosis, for inducing
 CC immunological tolerance, and for treating diseases curable or treatable
 CC by bone marrow transplantation, including leukemias, osteoporosis,
 CC aplastic anaemia, Gaucher's disease, and thalassemia. The present
 CC sequence represents recombinant immunotoxin, scFv(UCHT-1)-PE38
 XX SQ Sequence 601 AA;
 SQ Query Match 75.3%; Score 992; DB 6; Length 601;
 Best Local Similarity 78.8%; Pred. No. 9,1e-59;
 Matches 197; Conservative 12; Mismatches 35; Indels 6; Gaps 3;

ID AAU75382 standard; protein; 642 AA.
 XX AC AAU75382;
 XX AC AAU75382;
 XX DT 23-APR-2002 (first entry)
 XX DE Diphtheria toxin/UCHT1 immunotoxin fusion protein DT389.sfv(UCHT1).
 XX XX
 KM Immunotoxin; pseudomonas exotoxin A; ETA; diphtheria toxin; DT;
 KM cytosolic; immunosuppressive; immunostimulant; antidiabetic;
 KM antineumatic; antiarthritic; anti-HIV; anti-inflammatory;
 KM anti-T cell immunotoxin fusion protein; antibody; UCHT1;
 KM (GlySer)3 linker; T cell leukaemia; lymphoma; graft-versus-host disease;
 KM Fv; autoimmune disease; transplant rejection;
 KM systemic lupus erythematosus; type I diabetes; rheumatoid arthritis;
 KM myasthenia gravis; multiple sclerosis; AIDS; DT389.sfv(UCHT1);
 KM acquired immunodeficiency syndrome; chronic immunosuppression.
 XX XX
 OS Mus sp.
 OS Corynebacterium diphtheriae.
 OS Synthetic.
 OS Chimeric.
 XX PN WO200187982-A2.
 XX PD 22-NOV-2001.
 XX PF 18-MAY-2001; 2001WO-US016125.
 XX PR 18-MAY-2000; 2000US-00573797.
 XX PA (NOVS) NOVARTIS AG.
 XX PA (NOVS) NOVARTIS-ERINDUNGEN VERM GRS MBH.
 XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX PI Neville DM, Thompson JT, Hu H, Moo J, Ma S, Hexham JM, Digan ME;
 XX MPI; 2002-121980/16.
 XX DR N-PDSB; ABX13467.
 XX DR
 XX PT New anti-T cell immunotoxin fusion protein comprising a truncated
 PT diphtheria toxin moiety, a connector, and one single chain Fv of the
 PT variable region of a UCHT1 antibody, useful for treating e.g. autoimmune
 PT diseases.
 XX PS Claim 5; Fig 35; 307pp; English.
 XX CC The invention relates to an anti-T cell immunotoxin fusion protein,
 CC comprising from the amino terminus, a truncated diphtheria toxin moiety,
 CC a connector, and one single chain Fv of the variable region of a UCHT1
 CC antibody. The single chain Fv comprises VL, J, or VH. L is a Gly-Ser
 CC linker and VL and VH are the variable light and heavy domains of the
 CC anti-CD3 antibody UCHT1. Also included are a nucleic acid encoding the
 CC novel immunotoxin fusion protein, a vector comprising the nucleic acid
 CC and a cell comprising the nucleic acid. The immunotoxin may also be a
 CC pseudomonas endotoxin A (ETA). The immunotoxins are useful for treating T
 CC cell leukemias or lymphomas, graft-versus-host diseases, and autoimmune
 CC diseases by inducing immune tolerance. The immunotoxin fusion proteins
 CC may be used in vivo to systemically reduce populations of T cells, or ex
 CC vivo to effect T-cell depletion from a treated cell population. The
 CC fusion proteins can be administered to a subject who is or will be a
 CC recipient of an allotransplant to prevent or reduce T-cell mediated acute
 CC or chronic transplant rejection of the transplanted allogeneic cells,
 CC tissue or organ in the subject as well as treat other T-cell mediated
 CC diseases such as systemic lupus erythematosus, type I diabetes,
 CC rheumatoid arthritis, myasthenia gravis, multiple sclerosis, infectious
 CC diseases of the immune system (e.g. AIDS (acquired immunodeficiency
 CC syndrome)) and chronic immunosuppression. The present sequence is an
 CC immunotoxin fusion protein of the invention comprising 389 residues from
 CC the N-terminal glycine of mature DT toxin, a (GlySer)3 linker and one
 CC single Fv chain from antibody UCHT1, DT389.sfv(UCHT1)
 XX SQ Sequence 642 AA;

PI Neville DM, Thompson JT, Hu H, Woo J, Ma S, Hexham JM, Digan ME;
XX WPI; 2002-121980/16.
XX
XX New anti-T cell immunotoxin fusion protein comprising a truncated
PT diphtheria toxin moiety, a connector, and one single chain Fv of the
PT variable region of a UCHL1 antibody, useful for treating e.g. autoimmune
PT diseases.

PS Claim 7; Fig 34; 307pp; English.

XX The invention relates to an anti-T cell immunotoxin fusion protein,
XX comprising from the amino terminus, a truncated diphtheria toxin moiety,
CC a connector, and one single chain Fv of the variable region of a UCHL1
CC antibody. The single chain Fv comprises VL, L, or VH, L is a Gly-Ser
CC linker, and VL and VH are the variable light and heavy domains of the
CC anti-CD3 antibody UCHL1. Also included are a nucleic acid encoding the
CC novel immunotoxin fusion protein, a vector comprising the nucleic acid
CC and a cell comprising the nucleic acid. The immunotoxin may also be a
CC pseudomonas endotoxin A (ETA). The immunotoxins are useful for treating T
CC cell leukaemias or lymphomas, graft-versus-host diseases, and autoimmune
CC diseases by inducing immune tolerance. The immunotoxin fusion proteins
CC may be used in vivo to systemically reduce populations of T cells, or ex
CC vivo to effect T-cell depletion from a treated cell population. The
CC fusion proteins can be administered to a subject who is or will be a
CC recipient of an allograft transplant to prevent or reduce T-cell mediated acute
CC or chronic transplant rejection of the transplanted allogeneic cells,
CC tissue or organ in the subject as well as treat other T-cell mediated
CC diseases such as systemic lupus erythematosus, type I diabetes,
CC rheumatoid arthritis, myasthenia gravis, multiple sclerosis, infectious
CC diseases of the immune system (e.g. AIDS (acquired immunodeficiency
CC syndrome)) and chronic immunosuppression. The present sequence is an
CC immunotoxin fusion protein of the invention comprising 389 residues from
CC the N-terminal glycine of mature DT toxin, a (Gly458)3 linker and one
CC single Fv chain from antibody UCHL1, DT389.scfv (UCHL1)
XX

XX Sequence 643 AA;

Query March 75.3%; Score 992; DB 5; Length 643;
Best Local Similarity 78.8%; Pred. No. 9.8e-59;
Matches 197; Conservative 12; Mismatches 35; Indels 6; Gaps 3;

QY 1 DIQMTQTSSISASISAGDRTVSCRASQDIRNYLWYQKPDGTGKFLIYTSRLQPGVPS 60
DB 397 DIQMTQTSSISASISAGDRTVSCRASQDIRNYLWYQKPDGTGKFLIYTSRLHSGVPS 456
QY 61 RFSGSGSGTDYSLTINNLEQEDIGTFPCQCGNTPPMTFGGTGKLEIRGGSGSGGGSGG 120
DB 457 KFSGSGSGTDYSLTINNLEQEDIGTFPCQCGNTPPMTFGGTGKLEIRAGGGS--GGSGG 515
QY 121 GSGSGSGSEVQLQSGPELVKPGASVKISKDSGVAENSMWVWVKQPGQGLEWIGRIY 180
DB 516 G--SGGSEVQLQSGPELVKPGASVKISKASGYSTFGYTMWVWVKSHGKMLEMGLIN 573
QY 181 PGDDSNYNGKREGKALITADKSSSTAYMQLSSITVDSAVYFCARSGLL--RYANDY 237
DB 574 PYKGVSTYNGKREGKALITADKSSSTAYMQLSSITVDSAVYFCARSGYGDSDWYFDVW 633
QY 238 GQGTSTVTVSS 247
DB 634 GAGTTVTVSS 643

RESULT 15
AA029670
ID AA029670 standard; protein; 643 AA.
XX
XX AAO29670;
XX
XX 22-SEP-2003 (first entry)
XX
XX Anti-T cell immunotoxin fusion protein #1.
XX

KW Immunotoxin; anti-T cell; fusion protein; chemotherapeutic agent;
KW diphtheria toxin; Pseudomonas toxin; proliferative disease;
KW T-cell leukaemia; T-cell lymphoma; T-cell granular lymphatic leukaemia;
KW aggressive natural killer cell leukaemia; hairy-cell leukaemia;
KW Sezary syndrome; angioimmunoblastic T-cell lymphoma;
KW cutaneous T-cell lymphoma.
XX
XX Unidentified.
XX
XX WO2003045429-A2.
XX
XX 05-JUN-2003.
XX
XX 27-NOV-2002; 2002WO-BP013387.
XX
XX 28-NOV-2001; 2001GB-00028510.
XX
XX (NOVS) NOVARTIS AG.
XX (NOVS) NOVARTIS PHARMA GMBH.
XX
XX Engel G;
XX
XX WPI; 2003-482489/45.

DR Combination for treating malignant proliferative disease, e.g. leukemia
XX and lymphoma, has an anti-T cell immunotoxin fusion protein comprising a
PT diphtheria/Pseudomonas toxin and a targeting moiety, and a
PT chemotherapeutic agent.
XX
XX Claim 7; Page 23-27; 66pp; English.
XX
XX The invention relates to a novel combination comprising an anti-T cell
CC immunotoxin fusion protein and at least one chemotherapeutic agent. The
CC fusion protein comprises a diphtheria or Pseudomonas toxin moiety and a
CC targeting moiety suitable for targeting the fusion protein to T cells.
CC The novel combination is useful for preparing pharmaceutical composition
CC that is useful for delaying the progression of or for the treatment of a
CC malignant proliferative disease such as lymphoma or leukaemia in a
CC subject, in particular T-cell leukaemia, T-cell lymphoma, including T-
CC cell granular lymphatic leukaemia, aggressive natural killer cell
CC leukaemia, hairy-cell leukaemia, Sezary syndrome, angioimmunoblastic T-
CC cell lymphoma, peripheral T-cell lymphoma unspecified, cutaneous T-cell
CC lymphoma, subcutaneous panniculitis like T-cell lymphoma, and
CC hepatocellular carcinoma/delta T-cell lymphoma. The present sequence is an
CC example of anti-T cell immunotoxin fusion protein of the invention
XX

XX Sequence 643 AA;

Query March 75.3%; Score 992; DB 5; Length 643;
Best Local Similarity 78.8%; Pred. No. 9.8e-59;
Matches 197; Conservative 12; Mismatches 35; Indels 6; Gaps 3;

QY 1 DIQMTQTSSISASISAGDRTVSCRASQDIRNYLWYQKPDGTGKFLIYTSRLQPGVPS 60
DB 397 DIQMTQTSSISASISAGDRTVSCRASQDIRNYLWYQKPDGTGKFLIYTSRLHSGVPS 456
QY 61 RFSGSGSGTDYSLTINNLEQEDIGTFPCQCGNTPPMTFGGTGKLEIRGGSGSGGGSGG 120
DB 457 KFSGSGSGTDYSLTINNLEQEDIGTFPCQCGNTPPMTFGGTGKLEIRAGGGS--GGSGG 515
QY 121 GSGSGSGSEVQLQSGPELVKPGASVKISKDSGVAENSMWVWVKQPGQGLEWIGRIY 180
DB 516 G--SGGSEVQLQSGPELVKPGASVKISKASGYSTFGYTMWVWVKSHGKMLEMGLIN 573
QY 181 PGDDSNYNGKREGKALITADKSSSTAYMQLSSITVDSAVYFCARSGLL--RYANDY 237
DB 574 PYKGVSTYNGKREGKALITADKSSSTAYMQLSSITVDSAVYFCARSGYGDSDWYFDVW 633
QY 238 GQGTSTVTVSS 247
DB 634 GAGTTVTVSS 643

Thu Apr 22 14:51:00 2004

Search completed: April 22, 2004, 11:54:34
Job time : 53 secs

us-10-620-049-23.rag

Page 13

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OM protein - protein search, using sw model

Run on: April 22, 2004, 11:48:48 ; Search time 10.5 Seconds
(without alignments)
1224.888 Million cell updates/sec

Title: US-10-620-049-25

Perfect score: 1316

Sequence: 1 DIOMTQTSSLSASIGDRVT.....GLIRYAMDYMGQSTVTVSS 247

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	508	38.6	108	1	KVSK_MOUSE
2	507	38.5	108	1	KVSN_MOUSE
3	506	38.4	108	1	KVSL_MOUSE
4	498	37.8	108	1	KVSO_MOUSE
5	494	37.5	108	1	KVSM_MOUSE
6	473	35.9	108	1	KVSV_MOUSE
7	454	34.5	108	1	KVSO_MOUSE
8	443	33.7	140	1	HV02_MOUSE
9	440.5	33.5	139	1	HV07_MOUSE
10	430	32.7	120	1	HV03_MOUSE
11	426.5	32.1	117	1	HV11_MOUSE
12	423	32.0	117	1	HV06_MOUSE
13	421	31.8	118	1	HV13_MOUSE
14	419	31.5	117	1	HV18_MOUSE
15	415	31.5	121	1	HV01_MOUSE
16	414	31.4	117	1	HV12_MOUSE
17	413	30.9	118	1	HV05_MOUSE
18	406.5	30.8	117	1	HV04_MOUSE
19	405	30.6	117	1	HV04_MOUSE
20	403	30.6	117	1	HV04_MOUSE
21	400.5	30.4	120	1	HV05_MOUSE
22	395	30.0	108	1	KVSP_MOUSE
23	389	29.6	108	1	KV1Y_HUMAN
24	388	29.5	117	1	HV09_MOUSE
25	388	29.5	130	1	KVSG_MOUSE
26	382	29.0	117	1	HV49_MOUSE
27	379	28.8	108	1	KV1B_HUMAN
28	379	28.8	108	1	KV1O_HUMAN
29	379	28.8	117	1	HV10_MOUSE
30	378	28.7	108	1	KV1A_HUMAN
31	377	28.6	117	1	HV14_MOUSE
32	376	28.6	108	1	KV1P_HUMAN
33	376	28.6	108	1	KV1P_HUMAN

34	366	27.8	108	1	KV1H_HUMAN
35	366	27.8	108	1	KV1E_HUMAN
36	365	27.7	108	1	KV1E_HUMAN
37	365	27.7	128	1	KV1E_MOUSE
38	365	27.7	129	1	KV1M_HUMAN
39	364	27.7	108	1	KV1M_HUMAN
40	364	27.7	108	1	KV1Q_HUMAN
41	362	27.5	136	1	HV15_MOUSE
42	361	27.4	108	1	KV1C_HUMAN
43	361	27.4	108	1	KV1V_HUMAN
44	360	27.4	108	1	KV1G_HUMAN
45	356.5	27.1	147	1	HV1C_HUMAN

ALIGNMENTS

RESULT 1					
KVSK_MOUSE	STANDARD;	PRT;	108 AA.		
ID	KVSK_MOUSE				
AC	P01644;				
DT	21-JUL-1986 (Rel. 01, Created)				
DT	21-JUL-1986 (Rel. 01, Last sequence update)				
DT	28-FEB-2003 (Rel. 41, Last annotation update)				
DE	Ig kappa chain V-V region HP R16.7.				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
OX	NCBI_TaxID=10090;				
RN	[1]				
RP	SEQUENCE.				
RC	STRAIN=AJ/;				
RA	MEDLINE=82150934; PubMed=6801658;				
RX	Stegelman W.; Capra J.D.;				
RT	"Complete amino acid sequence of light chain variable regions derived from five monoclonal anti-p-azophenylarsenate antibodies differing with respect to a crossreactive idiotype."				
RT	Proc. Natl. Acad. Sci. U.S.A. 78:7679-7683(1981).				
CC	-1- MISCELLANEOUS: Anti-arsenate hybridoma protein.				
DR	PIR; A01927; KIMSAR.				
DR	HSSP; P01607; IREI.				
DR	InterPro; IPR007110; Ig-like.				
DR	InterPro; IPR003596; Ig_V.				
DR	Pfam; PF00047; Ig_1.				
DR	SMART; SMO0406; IgV_1.				
KM	PROSITE; PS00835; IG_LIKE; 1.				
FT	Immunoglobulin V region.				
FT	DOMAIN 1 23				
FT	DOMAIN 24 34				
FT	DOMAIN 35 49				
FT	DOMAIN 50 56				
FT	DOMAIN 57 88				
FT	DOMAIN 89 97				
FT	DOMAIN 98 108				
FT	DISULFID 23 88				
FT	NON_TER 108 108				
SQ	SEQUENCE 108 AA; A554642C63EFP597 CRC64;				
Query Match	38.6%; Score 508; DB 1; Length 108;				
Best Local Similarity	90.7%; Pred. No. 6.8e-33;				
Matches	98; Conservative 3; Mismatches 7; Indels 0; Gaps 0;				
QY	1 DIOMTQTSSLSASIGDRVTSCRASQPIRYILNMYQCKPGTYKFLIYNSRLPGVPS 60				
DB	1 DIOMTQTSSLSASIGDRVTISCRASQDISYLNMYQCKPGTYKFLIYNSRLHSGVPS 60				
QY	61 RPSGSGGTDSYSLTININLEQEDIGTFPCQGNTPPMTFGGQTKLEIKR 108				
DB	61 RPSGSGGTDSYSLTININLEQEDIGTFPCQGNTPPMTFGGQTKLEIKR 108				
RESULT 2					
KVSN_MOUSE					

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ID  KVEN_MOUSE  STANDARD;  PRT;  108 AA.
AC  P01647;
DT  21-JUL-1986 (Rel. 01, Created)
DT  21-JUL-1986 (Rel. 01, Last sequence update)
DT  28-FEB-2003 (Rel. 41, Last annotation update)
DE  Ig kappa chain V-V region HP 12481.
OS  Mus musculus (Mouse).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
XX  NCBI_TaxID=10090;
RN  [1]
RP  SEQUENCE.
RC  STRAIN=A/J;
RX  MEDLINE=82150934; PubMed=6801658;
RA  Siegelman M., Capra J.D.;
RT  "Complete amino acid sequence of light chain variable regions derived
RT  from five monoclonal anti-p-azophenylarsenate antibodies differing
RT  with respect to a crossreactive idioType."
RL  Proc. Natl. Acad. Sci. U.S.A. 78:7679-7683(1981).
CC  -1- MISCELLANEOUS: Anti-arsenate hybridoma protein.
DR  HSP; P01607; IREI.
DR  InterPro; IPR007110; IG-like.
DR  Pfam; PF00047; IG_1.
DR  SMART; SM00406; IGV; 1.
DR  PROSITE; PS50835; IG_LIKE; 1.
KW  Immunoglobulin V region.
FT  DOMAIN 1 23 34 49 56 66 77 88 97 108
FT  DOMAIN 2 24 34 49 56 66 77 88 97 108
FT  DOMAIN 3 24 34 49 56 66 77 88 97 108
FT  DOMAIN 4 24 34 49 56 66 77 88 97 108
FT  DISULFID 23 88
FT  NON TER 108 108
SQ  SEQUENCE 108 AA; 11965 MW; 399718C653EF58E CRC64;

Query Match
Best Local Similarity 90.7%; Score 507; DB 1; Length 108;
Matches 98; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

OY  1 DIOMTQTSSLSASIGDRVTVSCRASODIRNYLWYQOKPDGVKFLIYYSRLPGVPS 60
DB  1 DIOMTQTSSLSASIGDRVTVSCRASODIRNYLWYQOKPDGVKFLIYYSRLPGVPS 60
OY  61 RFSGSGSGTDYSLTINLEQEDIGTYFCQCGNTPTWFGGKLEIKR 108
DB  61 RFSGSGSGTDYSLTINLEQEDIGTYFCQCGNTPTWFGGKLEIKR 108

RESULT 3
KVSL_MOUSE  STANDARD;  PRT;  108 AA.
ID  KVSL_MOUSE  STANDARD;  PRT;  108 AA.
AC  P01645;
DT  21-JUL-1986 (Rel. 01, Created)
DT  21-JUL-1986 (Rel. 01, Last sequence update)
DT  28-FEB-2003 (Rel. 41, Last annotation update)
DE  Ig kappa chain V-V region HP 93G7.
OS  Mus musculus (Mouse).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
XX  NCBI_TaxID=10090;
RN  [1]
RP  SEQUENCE.
RC  STRAIN=A/J;
RX  MEDLINE=82150934; PubMed=6801658;
RA  Siegelman M., Capra J.D.;
RT  "Complete amino acid sequence of light chain variable regions derived
RT  from five monoclonal anti-p-azophenylarsenate antibodies differing
RT  with respect to a crossreactive idioType."
RL  Proc. Natl. Acad. Sci. U.S.A. 78:7679-7683(1981).
CC  -1- MISCELLANEOUS: Anti-arsenate hybridoma protein.

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DR  HSP; P01607; IREI.
DR  InterPro; IPR007110; IG-like.
DR  InterPro; IPR003596; IG_v.
DR  Pfam; PF00047; IG_1.
DR  SMART; SM00406; IGV; 1.
DR  PROSITE; PS50835; IG_LIKE; 1.
KW  Immunoglobulin V region.
FT  DOMAIN 1 23 34 49 56 66 77 88 97 108
FT  DOMAIN 2 24 34 49 56 66 77 88 97 108
FT  DOMAIN 3 24 34 49 56 66 77 88 97 108
FT  DOMAIN 4 24 34 49 56 66 77 88 97 108
FT  DISULFID 23 88
FT  NON TER 108 108
SQ  SEQUENCE 108 AA; 11954 MW; 22F4642C63EF58E CRC64;

Query Match
Best Local Similarity 90.7%; Score 506; DB 1; Length 108;
Matches 98; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

OY  1 DIOMTQTSSLSASIGDRVTVSCRASODIRNYLWYQOKPDGVKFLIYYSRLPGVPS 60
DB  1 DIOMTQTSSLSASIGDRVTVSCRASODIRNYLWYQOKPDGVKFLIYYSRLPGVPS 60
OY  61 RFSGSGSGTDYSLTINLEQEDIGTYFCQCGNTPTWFGGKLEIKR 108
DB  61 RFSGSGSGTDYSLTINLEQEDIGTYFCQCGNTPTWFGGKLEIKR 108

RESULT 4
KVSO_MOUSE  STANDARD;  PRT;  108 AA.
ID  KVSO_MOUSE  STANDARD;  PRT;  108 AA.
AC  P01648;
DT  21-JUL-1986 (Rel. 01, Created)
DT  21-JUL-1986 (Rel. 01, Last sequence update)
DT  28-FEB-2003 (Rel. 41, Last annotation update)
DE  Ig kappa chain V-V region HP 91A3.
OS  Mus musculus (Mouse).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
XX  NCBI_TaxID=10090;
RN  [1]
RP  SEQUENCE.
RC  STRAIN=A/J;
RX  MEDLINE=82150934; PubMed=6801658;
RA  Siegelman M., Capra J.D.;
RT  "Complete amino acid sequence of light chain variable regions derived
RT  from five monoclonal anti-p-azophenylarsenate antibodies differing
RT  with respect to a crossreactive idioType."
RL  Proc. Natl. Acad. Sci. U.S.A. 78:7679-7683(1981).
CC  -1- MISCELLANEOUS: Anti-arsenate hybridoma protein.
DR  HSP; P01607; IREI.
DR  InterPro; IPR007110; IG-like.
DR  InterPro; IPR003596; IG_v.
DR  Pfam; PF00047; IGV; 1.
DR  SMART; SM00406; IGV; 1.
DR  PROSITE; PS50835; IG_LIKE; 1.
KW  Immunoglobulin V region.
FT  DOMAIN 1 23 34 49 56 66 77 88 97 108
FT  DOMAIN 2 24 34 49 56 66 77 88 97 108
FT  DOMAIN 3 24 34 49 56 66 77 88 97 108
FT  DOMAIN 4 24 34 49 56 66 77 88 97 108
FT  DISULFID 23 88
FT  NON TER 108 108
SQ  SEQUENCE 108 AA; 11961 MW; D528DA5E9A45291C CRC64;

Query Match
Best Local Similarity 86.9%; Score 498; DB 1; Length 108;
Matches 98; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

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Matches 96; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 1 DIOMTQTSSLSASLGRTVSCRASODIRNYLWYQOKPDGTVKFLIYTSRLPGVPS 60
 DB 1 DIOMTQTSSLSASLGRTVSCRASODIRNYLWYQOKPDGTVKFLIYTSRLPGVPS 60
 QY 61 RFSGSGGSDYSLTINNLEQEDIGTYFCQCGNTPTPFGGCTKLEIKR 108
 DB 61 RFSGSGGSDYSLTINNLEQEDIGTYFCQCGNTPTPFGGCTKLEIKR 108

RESULT 5

KVSM_MOUSE STANDARD; PRT; 108 AA.
 AC P01646;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE IG kappa chain V-V region HP 123B6.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=A/J;
 RX MEDLINE=62150934; PubMed=6801658;
 RA Siegelman M., Capra J.D.;
 RT "Complete amino acid sequence of light chain variable regions derived
 from five monoclonal anti-p-azophenylarsenate antibodies differing
 with respect to a crossreactive idiotype.";
 RL Proc. Natl. Acad. Sci. U.S.A. 78:7679-7683 (1981).
 CC -1- MISCELLANEOUS: Anti-arsenate hybridoma protein.
 DR HSP; P01607; IREI.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF00047; IG; 1.
 DR SMART; SM00406; IG; 1.
 DR PROSITE; PS50835; IG LIKE; 1.
 KW Immunoglobulin V region.

FT DOMAIN 1 23 FRAMEWORK-1.
 FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 35 49 FRAMEWORK-2.
 FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 57 88 FRAMEWORK-3.
 FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
 FT DOMAIN 98 108 FRAMEWORK-4.
 FT DISULFID 23 88 BY SIMILARITY.
 FT NON_TER 108
 SQ SEQUENCE 108 AA; 11989 MW; 4C98599C08BBA09A CRC64;

Query Match 37.5%; Score 494; DB 1; Length 108;
 Best Local Similarity 88.9%; Pred. No. 8.2e-32;
 Matches 96; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 1 DIOMTQTSSLSASLGRTVSCRASODIRNYLWYQOKPDGTVKFLIYTSRLPGVPS 60
 DB 1 DIOMTQTSSLSASLGRTVSCRASODIRNYLWYQOKPDGTVKFLIYTSRLPGVPS 60
 QY 61 RFSGSGGSDYSLTINNLEQEDIGTYFCQCGNTPTPFGGCTKLEIKR 108
 DB 61 RFSGSGGSDYSLTINNLEQEDIGTYFCQCGNTPTPFGGCTKLEIKR 108

RESULT 6

KVSV_MOUSE STANDARD; PRT; 108 AA.
 AC P04946;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG kappa chain V-V region NQ5-89.4.
 OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=83271467; PubMed=6877353;
 RA Kaartinen M., Griffiths G.M., Markham A.F., Milstein C.;
 RT "mRNA sequences define an unusually restricted IgG response to 2-
 phenylloxazoline and its early diversification.";
 RL Nature 304:320-324 (1983).
 CC -1- MISCELLANEOUS: ANTI-2-PHENYL OXAZOLONE (PROX) ANTIBODY.
 CC -----
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CC EMBL; K00745; AA38690.1; -.
 DR HSP; P01607; IREI.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF00047; IG; 1.
 DR SMART; SM00406; IG; 1.
 DR PROSITE; PS50835; IG LIKE; 1.
 KW Immunoglobulin V region; Hybridoma.
 FT DOMAIN 1 23 FRAMEWORK-1.
 FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 35 49 FRAMEWORK-2.
 FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 57 88 FRAMEWORK-3.
 FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
 FT DOMAIN 98 107 FRAMEWORK-4.
 FT DISULFID 23 88 BY SIMILARITY.
 FT NON_TER 108
 SQ SEQUENCE 108 AA; 11866 MW; DB2C885920DC6DD CRC64;

Query Match 35.9%; Score 473; DB 1; Length 108;
 Best Local Similarity 84.3%; Pred. No. 3.4e-30;
 Matches 91; Conservative 4; Mismatches 13; Indels 0; Gaps 0;

QY 1 DIOMTQTSSLSASLGRTVSCRASODIRNYLWYQOKPDGTVKFLIYTSRLPGVPS 60
 DB 1 DIOMTQTSSLSASLGRTVSCRASODIRNYLWYQOKPDGTVKFLIYTSRLPGVPS 60
 QY 61 RFSGSGGSDYSLTINNLEQEDIGTYFCQCGNTPTPFGGCTKLEIKR 108
 DB 61 RFSGSGGSDYSLTINNLEQEDIGTYFCQCGNTPTPFGGCTKLEIKR 108

RESULT 7

KVSV_MOUSE STANDARD; PRT; 108 AA.
 AC P01643;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG kappa chain V-V region MOPC 173.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=76091934; PubMed=812636;
 RA Schiff C., Fougereau M.;
 RT "Determination of the primary structure of a mouse IgG2a
 immunoglobulin. Amino-acid sequence of the light chain.";
 RL Eur. J. Biochem. 59:525-537 (1975).
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
 DR PIR; A01926; KMS73.

DR HSSP; P01607; 1RE1.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003596; IG-V.
 DR Pfam; PF00047; IG; 1.
 DR SMART; SM00406; IG; 1.
 DR PROSITE; PS50835; IG LIKE; 1.
 KW Immunoglobulin V region.
 FT DOMAIN 1 23
 FT DOMAIN 24 34
 FT DOMAIN 35 49
 FT DOMAIN 50 56
 FT DOMAIN 57 88
 FT DOMAIN 89 97
 FT DOMAIN 98 108
 FT DISULFID 23 88
 FT NON TER 108
 SQ SEQUENCE 108 AA; 11819 MM; 2AD23D92A72AA0A3 CRC64;

Query Match 34.5%; Score 454; DB 1; Length 108;
 Best Local Similarity 79.6%; Pred. No. 1e-28;
 Matches 86; Conservative 9; Mismatches 13; Indels 0; Gaps 0;

QY 1 DIQWQTSSLSASIGDVTVCASODIRNYLNMWQKPDGTVKFLIYTSRLPVPVS 60
 DB 1 DIQWQTSSLSASIGDVTVCASODIRNYLNMWQKPDGTVKFLIYTSRLPVPVS 60
 QY 61 RFGSGSGTGYSLTINLEQEDIGTFQCGQNTPTPTGGTKEIKR 108
 DB 61 RFGSGSGTGYSLTINLEQEDIGTFQCGQNTPTPTGGTKEIKR 108

RESULT 8
 HV02_MOUSE STANDARD; PRT; 140 AA.
 ID P01746;
 AC 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DE 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Ig heavy chain V region 9367 precursor.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A/J;
 RX MEDLINE=82152818; PubMed=6801765;
 RA Sims U., Rabbits T.H., Estees P., Slaughter C., Tucker P.W.,
 RA Capra J.D.;
 RT "Somatic mutation in genes for the variable portion of the
 immunoglobulin heavy chain";
 RL Science 216:309-311(1982).
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
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 or send an email to license@isb-sib.ch).
 CC EMBL; J00493; AAA38128.1; -
 DR PIR; A94264; HVMG7.
 DR HSSP; P01810; 2FBJ.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003596; IG-V.
 DR Pfam; PF00047; IG; 1.
 DR SMART; SM00406; IG; 1.
 DR PROSITE; PS50835; IG-LIKE; 1.
 KW Immunoglobulin V region; Hybridoma; Signal.
 FT SIGNAL 1 19
 FT CHAIN 20 140 IG HEAVY CHAIN V REGION 9367.

FT DOMAIN 20 139 IG-LIKE.
 FT NON TER 140
 SQ SEQUENCE 140 AA; 15514 MM; 25A4CBBE31DA5CE8 CRC64;

Query Match 33.7%; Score 443; DB 1; Length 140;
 Best Local Similarity 70.9%; Pred. No. 9.6e-28;
 Matches 90; Conservative 8; Mismatches 27; Indels 2; Gaps 1;

QY 123 SCGSGSEVOLQSGELVKGASVXISCKDSGYAFNSMNMVVKORPGQLEWIGRIYPG 182
 DB 14 TAGVHSEVQLQSGALVLRAGSVMSCKAGYTTSTYGINVMVQRPQGLEWIGIYNG 73
 QY 183 DDDSNNGKFBGKAILI7DKSSSTIYNQLSLTVSDSVYFCASGGLL--RYANDYNGQ 240
 DB 74 NGYINYNKFKGKTYLTVDKSSSTIYNQLSLTVSDSVYFCARSHYGGSDYDFYWGQ 133
 QY 241 TSVTVSS 247
 DB 134 TPLTVSS 140

RESULT 9
 HV07_MOUSE STANDARD; PRT; 139 AA.
 ID HV07_MOUSE
 AC P01751; P01752;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DE 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Ig heavy chain V region B1-8/186-2 precursor.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6;
 RX MEDLINE=81234548; PubMed=6788376;
 RA Botwell A.L.M., Paskind M., Rath M., Imanishi-Kari T., Rajewsky K.,
 RA Baltimore D.;
 RT "Heavy chain variable region contribution to the NPB family of
 antibodies: somatic mutation evident in a gamma 2a variable region";
 RL Cell 24:625-637(1981).
 CC -1- MISCELLANEOUS: THE B1-8 MU CHAIN MRNA WAS CLONED FROM A HYBRIDOMA
 MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
 (NPB ANTIBODIES).
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 or send an email to license@isb-sib.ch).
 CC EMBL; J00529; AAA38170.1; -
 DR PIR; A90809; MEMS18.
 DR PDB; 1A6U; 27-MAY-98.
 DR PDB; 1A6W; 15-JUL-98.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003596; IG-V.
 DR Pfam; PF00047; IG; 1.
 DR SMART; SM00406; IG; 1.
 DR PROSITE; PS50835; IG-LIKE; 1.
 KW Immunoglobulin V region; Signal; 3D-structure.
 FT SIGNAL 1 19
 FT CHAIN 20 139 IG HEAVY CHAIN V REGION B1-8/186-2.
 FT DOMAIN 20 49
 FT DOMAIN 50 54
 FT DOMAIN 55 68
 FT DOMAIN 69 85
 FT DOMAIN 86 117
 FT DOMAIN 118 124
 FT DOMAIN 125 139
 D SEGMENT.
 JH2 SEGMENT.

Thu Apr 22 14:51:04 2004

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	DISULFID	41	115	BY SIMILARITY.	
FT	NON TER	139	139		
SQ	SEQUENCE	139 AA;	15419 MW;	1B57DD4F00C9P465 CRC64;	
	Query Match		33.5%;	Score 440.5; DB 1;	Length 139;
	Best Local Similarity		70.2%;	Pred. No. 1.5e-27;	
	Matches	87;	Conservative 10;	Mismatches 26;	Indels 1;
Oy		125	GGGSEVQCQGSGPELVKPGASVKISCKDGYAFNSMMWVKORPGCGLEWIGRIYPDG	184	
Dd		16	GHSQYVQCQGGALVELKVGASVKLSCKASGTFTSYMHVMWKQRGRGLEWIGRIDPMSG	75	
Oy		185	DSNTNGKEEGKAILTFADKSSSTAYNQSLTSDSAVVFCAKSGLLRA--MDYMGCGTSV	243	
Dd		76	GTRKNKKRSKATLTFVDKPSSTAYNQSLTSEDSDAVVCARYDYGGSYDFYMQGGITL	135	
Oy		244	TVSS 247		
Dd		136	TVSS 139		
	RESULT 10				
HV03_MOUSE					
ID	HV03_MOUSE	STANDARD;	PRT;	120 AA.	
AC	P01747;				
DT	21-JUL-1986 (Rel. 01, Created)				
DT	21-JUL-1986 (Rel. 01, Last sequence update)				
DT	10-OCT-2003 (Rel. 42, Last annotation update)				
DE	Ig heavy chain V region 36-65.				
OS	Mus musculus (Mouse).				
CC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
CC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
OX	NCBI_Taxid=10090;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=83313646; PubMed=6186498;				
RA	Stekvez M., Gelfer M.L., Brodeur P., Riblet R.,				
RA	Marbach-Rothstein A.;				
RT	"The genetic basis of antibody production: the dominant anti-arsonate				
RT	idiotype response of the strain A mouse.";				
RL	Eur. J. Immunol. 12:1023-1032(1982).				
CC	- MISCELLANEOUS: FROM ANALYSIS OF THE SIZES OF SEVERAL OTHER				
CC	DIFERENTIATED GENES THAT HYBRIDIZE TO THIS ONE, THE AUTHORS				
CC	CONCLUDE THAT ALL OF THESE V REGIONS HAVE REARRANGED TO THE SAME J				
CC	SEGMENT, JH2.				
CC	-I- SIMILARITY: Contains 1 immunoglobulin-like domain.				
DR	HSSP; P01789; IMCP.				
DR	InterPro; IPR007110; Ig-like.				
DR	InterPro; IPR003596; IG_v.				
DR	pfam; PF00047; Ig_1.				
DR	SMART; SM00406; IGV_1.				
DR	PROSITE; PS00835; IG-LIKE_1.				
KM	Immunoglobulin V region; Hybridoma.				
FT	DOMAIN	1	111	IG-LIKE.	
FT	NON TER	120	120		
SQ	SEQUENCE	120 AA;	13307 MW;	FF04E4A167B654AE CRC64;	
	Query Match		32.7%;	Score 430; DB 1;	Length 120;
	Best Local Similarity		71.7%;	Pred. No. 8.1e-27;	
	Matches	86;	Conservative 9;	Mismatches 23;	Indels 2;
Oy		130	VQLQSGPELVKPGASVKISKDGYAFNSMMWVKORPGCGLEWIGRIYPDGSDNN	169	
Dd		1	VVLQSGSGLVLRKSSSVKMSCKASGTFTSYGNVAKRQGGLEWIGRIINPANGITKIN	60	
Oy		190	GKEEGKAILTFADKSSSTAYNQSLTSDSAVVFCAKSGLL--RYANDYGCGTSTVSS	247	
Dd		61	EKKKGKTLTFVDKSSSTAYNQSLTSEDSDAVVCARYDYGGSYDFYMQGGITLTVSS	120	

[illegible]

DR	EMBL;	J00599;	AAA8172.1;	-.
DR	PIR;	A02038;	G2MG43.	
DR	HSSP;	P01810;	2FBJ.	
DR	InterPro;	IPR007110;	IG-like.	
DR	InterPro;	IPR003596;	IG_v.	
DR	Pfam;	PF00047;	Ig; 1.	
DR	SMART;	SM00405;	Ig; 1.	
DR	PROSITE;	PS50835;	Ig_Like; 1.	
KW	Immunoglobulin V region;	Signal.		
FT	SIGNAL	1	19	
FT	CHAIN	20	137	
FT	DOMAIN	20	49	
FT	DOMAIN	50	54	
FT	DOMAIN	55	68	
FT	DOMAIN	69	85	
FT	DOMAIN	86	117	
FT	DOMAIN	118	122	
FT	DOMAIN	123	137	
FT	DISULFID	41	115	
FT	NON_TER	137	137	
SQ	SEQUENCE	137 AA;	15200 MW; ADD5881BF4ABEC9 CRC64;	
<hr/>				
Query Match		32.4%;	Score 426.5; DB 1; Length 137;	
Best Local Similarity		69.9%;	Pred. No. 1.8e-26;	
Matches	86; Conservative		8; Mismatches 28; Indels 1; Gaps 1	
<hr/>				
Dy	125	GGGSEYVQLDQSGPELVKPGASVKISCKSPGVAFNSMMNWVRQPGQGLEWIGRIYPGDG	184	
		:::: :	:	
Dy	16	GVHSQVLQQPGAEVKKPKASVKLSCKAGSYFTSLHWNVQRGRGLGEWIGRIDENSG	75	
		:	:	
Oy	185	DSNYNKEFEKGKAILTKADKSSATYNQLSLITVDSDAVYFCASGLIRYMNDWGQTSTVT	244	
		:	:	
Dy	76	GIPTVNHFFRSKATLLTIDKPSSTAYNQLSLTSEDSDAIVYCARYPLGRY-FDIWGGGTTLT	134	
		:	:	
Oy	245	VSS 247		
		:		
Dy	135	VSS 137		
<hr/>				
RESULT 12				
HVS2_MOUSE				
ID	HVS2_MOUSE	STANDARD;	FRT;	117 AA.
AC	P06327;			
DT	01-JAN-1988 (Rel. 06, Created)			

DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DT Ig heavy chain V region VH558 A1/A4 precursor.
DE Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=8509340; PubMed=2578321;
RA Yancopoulos G.D.; Alt F.W.;
RT "Developmentally controlled and tissue-specific expression of
RT unarranged VH gene segments.";
RL Cell 40:271-281(1985).
CC -----
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DR	EMBL; M13787; AAA8499.1; -.
DR	PIR; A02029; HVMSA1.
DR	HSSP; P01810; 2PBJ.
DR	InterPro; IPR007110; IG-like.
DR	InterPro; IPR003596; IG_v.
DR	Pfam; PF00047; 4G.1.
DR	SMART; SMO0406; IGV.1.
DR	ProSITE; PS0835; IG_LIKE; 1.
KW	immunoglobulin V region; Signal.
FT	SIGNAL 1 19
FT	CHAIN 20 117
FT	DOMAIN 20 49
FT	DOMAIN 50 54
FT	DOMAIN 55 68
FT	DOMAIN 69 85
FT	DOMAIN 86 117
FT	DISULFID 41 115
FT	NON_TER 117 117
SQ	SEQUENCE 117 AA; 12971 MW; 8B0BC138856DFC9D CRC64;

	Query Match	Similarity	Score	DB 1	Length
Best Local	83	79.0%	423	DB 1	117
Matches	83	Conservative	6	Mismatches	16
				Indels	0
				Gaps	0

	Query	Match	Similarity	Score	DB 1	Length
Qy	122 GAGGGGSAVYQLOOQSPRLVYKPGASVYKTSCKDQGVAFNNSMMWVYQRPQGLWETIGRTYP	181				
	13 GAGVHCQVQLOQSPRLVYKPGALYKTSCKAGYFTSTVDIMWVQRPQGLWETIGRTYP	72				
Db	182 GQDSNINYSKFEKKAILLTADKSSSTAYWQLSLTSDYDAVYTCAR	226				
Qy	73 GQGSRTYNEKEFKGKATLLTADKSSSTAYWQLSLTSDYDAVYTCAR	117				
Db						

	RESULT	13
HV06_MOUSE		
ID_HV06_MOUSE	STANDARD;	PRT; 117 AA.
P01750;		
DT 21-JUL-1986	(Rel. 01,	Created)
DT 21-JUL-1986	(Rel. 01,	Last sequence update)
DT 15-JUL-1999	(Rel. 38,	Last annotation update)
DE Ig heavy chain V region 102 precursor.		
OS Mus musculus (Mouse).		
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus		
OX NCBI_Taxid=10090;		
RN [1]		
RP SEQUENCE FROM N.A.		
RC STRAIN=C57BL/6;		
RX MEDLINE=G1234549; PubMed=6788376;		
RA Buchwal1 A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky J		

RA	Baltimore D.;
RT	"Heavy chain variable region contribution to the Npb family of antibodies; somatic mutation evident in a gamma 2a variable region.";
RL	Cell 24:625-637(1981).
CC	-1 MISCELLANEOUS; THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
DR	PIR; A02032; HVMS02.
DR	HSSP; P01810; ZEBJ.
DR	InterPro; IPR007110; IG-like.
DR	InterPro; IPR003596; IG_v.
DR	Pfam; PF00047; Ig; 1.
DR	SMART; SMO0406; IgV; 1.
DR	PROSITE; PSS08035; IG LIKE; 1.
KW	Immunoglobulin V region; signal.
FT	SIGNAL
FT	CHAIN
FT	DOMAIN
FT	DOMAIN
FT	DOMAIN
FT	DOMAIN
FT	DOMAIN
FT	DISULFID
FT	NON_TER
SQ	SEQUENCE
	117 AA; 12867 MW; 740A65DBD851C8AC CRC64;

	Query Match	Similarity	Score	DB 1	Length
Best Local	80%	79.2%	421	DB 1	117
Matches	80	Conservative	6	Mismatches	15
				Indels	0
				Gaps	0

RESULT 14			
HY48_MOUSE			
ID	HY48_MOUSE	STANDARD:	PRT: 138 AA.
AC	P03980:		
DT	23-OCT-1986 (Rel. 02, Created)		
DT	23-OCT-1986 (Rel. 02, Last sequence update)		
DT	15-JUL-1993 (Rel. 38, Last annotation update)		
DE	I9 heavy chain V region TIEPC 1017 precursor.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCBI_TaxID=10090;		

RP	SEQUENCE FROM N.A.		
RX	MEDLINE=84248078; PubMed=6429663;		
RA	Gilliam A.C., Shan A., Richards J.E., Blattner F.R., Mushinski J.F.,		
RA	Tucker P.W.;		
RT	"illegitimate recombination generates a class switch from C mu to C		
RT	delta in an IgD-secreting plasmacytoma."		
RL	Proc. Natl. Acad. Sci. U.S.A. 81:4164-4168(1984).		
RL	Pir, A0203; HEMST7.		
DR	HSE, P01810; HSEBU.		
DR	InterPro; IPR007110; IG-1like.		
DR	InterPro; IPR003596; IG_v.		
DR	Pfam; PF00047; IG_1.		
DR	SMART; SMO0406; IGV; 1.		
DR	PROSITE; PS50835; IG_LIKE; 1.		
KW	Immunoglobulin V region; Signal.		
FT	SIGNAL	1	20
FT	CHAIN	21	138
FT	DOMAIN	51	49
FT	DOMAIN	50	54
FT	DOMAIN	55	68
FT	DOMAIN	69	85
FT	DOMAIN	86	117
			IG HEAVY CHAIN V REGION TEPC 1017.
			FRAMEWORK-1.
			COMPLEMENTARITY-DETERMINING-1.
			FRAMEWORK-2.
			COMPLEMENTARITY-DETERMINING-2.
			FRAMEWORK-3.

FT DOMAIN 118 127 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 128 138 FRAMEWORK-4.
FT DISULFID 41 115 BY SIMILARITY.
FT NON TER 138 138
SQ SEQUENCE 138 AA; 15576 MW; 74815734C6907B8E CRC64;

Query Match 31.8%; Score 419; DB 1; Length 138;
Best Local Similarity 68.3%; Pred. No. 6,7e-26;
Matches 82; Conservative 11; Mismatches 27; Indels 0; Gaps 0;

QY 128 SEVQLQDSGPGLPKGASVKISCKDQSGYAFNPSMMWVKORPQGLRWIGRIYPGDSDN 187
DB 19 SEVQLQDSGPGLPKGASVKISCKDQSGYAFNPSMMWVKORPQGLRWIGRIYPGDSDN 78
QY 188 YNKEFKKATLTVDKSSSTAYMQLSSLTYSVDSAVYFCARSGLRVMDYWGQSTVTVSS 247
DB 79 YNKEFKKATLTVDKSSSTAYMQLSSLTYSVDSAVYFCARSGLRVMDYWGQSTVTVSS 138

RESULT 15

HV13_MOUSE STANDARD; PRT; 117 AA.
ID HV13_MOUSE
AC P01757;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region J558.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=80078170; PubMed=6765983;
RA Schilling J., Clevinger B., Davie J.M., Hood L.;
RT "Amino acid sequence of homogeneous antibodies to dextran and DNA
rearrangements in heavy chain V-region gene segments."
RL Nature 283:35-40(1980).
CC -1- MISCELLANEOUS: THE SEQUENCES OF 10 HYBRIDOMA PROTEINS THAT ALSO
CC BIND DEXTRAN DIFFER FROM THAT SHOWN AT 1-7 POSITIONS, MANY OF
CC WHICH OCCUR IN THE D AND J SEGMENTS.
CC -1- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
CC -1- SIMILARITY: Contains 1 Immunoglobulin-like domain.
DR PIR; A26242; MMSUS.
DR HSSP; P01789; IMCP.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; Ig_1.
DR PROSITE; PS50835; Ig_LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 116 IG-LIKE.
FT DISULFID 22 96 BY SIMILARITY.
FT NON TER 117 117
SQ SEQUENCE 117 AA; 13024 MW; 292E2AF4BE447E41 CRC64;

Query Match 31.5%; Score 415; DB 1; Length 117;
Best Local Similarity 70.0%; Pred. No. 1.1e-25;
Matches 84; Conservative 10; Mismatches 22; Indels 4; Gaps 2;

QY 129 EVQLQDSGPGLPKGASVKISCKDQSGYAFNPSMMWVKORPQGLRWIGRIYPGDSDNY 188
DB 1 EVQLQDSGPGLPKGASVKISCKDQSGYAFNPSMMWVKORPQGLRWIGRIYPGDSDNY 60
QY 189 NGRFEGKATLTADKSSSTAYMQLSSLTYSVDSAVYFCARSGLRVMDYWGQSTVTVSS 247
DB 61 NGRFEGKATLTADKSSSTAYMQLSSLTYSVDSAVYFCARSGLRVMDYWGQSTVTVSS 117

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OW protein - protein search, using sw model

Run on: April 22, 2004, 11:49:33 ; Search time 36 Seconds
(without alignments)
2164.805 Million cell updates/sec

Title: US-10-620-049-25
Perfect score: 1316
Sequence: 1 DIOMTGTSTLSASLGDRTV.....GLLRVMDYWGQGTSTVTVSS 247

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : SPTRMBL_25:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phase:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriophage:*
- 17: sp_archaea:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Length	DB ID	Description
1	535	40.7	614	11	Q7TMT6 mus musculus
2	524.5	39.9	234	11	Q91WF8 mus musculus
3	486	36.9	111	11	Q9D9B8 mus musculus
4	483.5	36.7	110	11	Q9JL83 mus musculus
5	478	36.3	474	11	Q8R3H6 mus musculus
6	477.5	36.3	233	11	Q91WS9 mus musculus
7	471	35.8	142	11	Q924Q1 mus musculus
8	470	35.7	481	11	Q91WT1 mus musculus
9	469.5	35.7	145	11	Q924Q6 mus musculus
10	465.5	35.4	145	11	Q924Q9 mus musculus
11	464.5	35.3	145	11	Q924R1 mus musculus
12	464.5	35.3	145	11	Q924R4 mus musculus
13	464.5	35.2	118	11	Q921C4 mus musculus
14	461	35.0	146	11	Q924Q3 mus musculus
15	459.5	34.9	234	11	Q8R062 mus musculus
16	459.5	34.9	482	11	Q8K172 mus musculus

17	458.5	34.8	145	11	Q924P7 mus musculus
18	458	34.8	473	11	Q9D8L4 mus musculus
19	456.5	34.7	143	11	Q924R0 mus musculus
20	455.5	34.6	488	11	Q8K0F2 mus musculus
21	454	34.5	140	11	Q924R2 mus musculus
22	452	34.3	146	11	Q924R8 mus musculus
23	450.5	34.2	613	11	Q8VCX7 mus musculus
24	449.5	34.2	143	11	Q924Q0 mus musculus
25	446	33.9	117	11	Q9QX69 mus musculus
26	446	33.9	480	11	Q8K0Z4 mus musculus
27	445.5	33.9	473	11	Q9JL25 mus musculus
28	444	33.7	168	11	Q8VDC9 mus musculus
29	440.5	33.5	143	11	Q924P9 mus musculus
30	440	33.4	140	11	Q924P8 mus musculus
31	439.5	33.4	137	11	Q924R5 mus musculus
32	439	33.4	146	11	Q924Q8 mus musculus
33	436.5	33.2	141	11	Q924Q4 mus musculus
34	436.5	33.2	463	11	Q991C4 mus musculus
35	436	33.1	142	11	Q924Q2 mus musculus
36	435.5	33.1	145	11	Q924Q7 mus musculus
37	435	33.1	144	11	Q924P5 mus musculus
38	433.5	32.9	136	11	Q7TPE3 mus musculus
39	433	32.9	470	11	Q7TMK1 mus musculus
40	432.5	32.9	110	11	Q9JL77 mus musculus
41	431.5	32.8	143	11	Q924P6 mus musculus
42	430.5	32.7	145	11	Q924R3 mus musculus
43	429.5	32.6	143	11	Q924Q5 mus musculus
44	428.5	32.6	143	11	Q924R7 mus musculus
45	428.5	32.6	243	11	Q7TQM2 mus musculus

ALIGNMENTS

RESULT 1

ID Q7TMT6 PRELIMINARY; PRT; 614 AA.

AC Q7TMT6; 01-OCT-2003 (TREMBLrel. 25, Created)
 DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Hypothetical protein.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_Taxid=10090;
 RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6NCR; TISSUE=Hematopoietic Stem Cell;
 RX MEDLINE=22388257; PubMed=12477932;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klauener R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshblyuk S., Carlinici P., Prange C.,
 RA Raha S.S., Loggiano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.O., Malek J.A., Gnatrante P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalobos D.K., Muzny K.C., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.,
 RA Kravitz M.I., Skalska U., Smalins D.E., Scherch A., Schein J.E.,
 RA Jones S.J., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]

RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6NCR; TISSUE=Hematopoietic Stem Cell;

RA Strausberg R.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
RW EMBL; BC053409; RAH53409.1; -.
KW Hypothetical protein.
SQ SEQUENCE 614 AA; 67746 MW; 839BAF3B8D124F89 CRC64;

Query Match 40.7%; Score 535; DB 11; Length 614;
Best Local Similarity 82.9%; Pred. No. 5e-37; 14; Indels 0; Gaps 0;
Matches 102; Conservative 7; Mismatches 14; Indels 0; Gaps 0;
QY 125 GGGSEVQLQSGPGLVFKPGASVKISKDSGYAFNSMNMVVKQRPQGGLWIGRIYFGDG 184
DB 16 GVHSQVLQSGPGLVFKPGASVKISKDSGYAFNSMNMVVKQRPQGGLWIGRIYFGDG 75
QY 185 DSNYNGKFKGKAILTADKSSSTAYMQLSLTSDSAVFCARSGLLRYAMDYWGCGTSTV 244
DB 76 DTNYNGKFKGKATLTADKSSSTAYMQLSLTSDSAVFCARDYSGSYFYAWGCGTLVT 135
QY 245 VSS 247
DB 136 VSA 138

RESULT 2
Q91WF8 PRELIMINARY; PRT; 234 AA.
ID Q91WF8
AC Q91WF8
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon;
RA Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC015292; AAH15292.1; -.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0005840; C:ribosome; IEA.
DR GO; GO:0003735; F:structural constituent of ribosome; IEA.
DR GO; GO:0006412; F:protein biosynthesis; IEA.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Ribosomal_S2.
DR SMART; SM00406; Ig; 1.
DR PROSITE; PS00835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; 1.
DR PROSITE; PS00962; RIBOSOMAL_S2_1; 1.
KW Hypothetical protein.
SQ SEQUENCE 234 AA; 25929 MW; B0D0B056EB7812D2 CRC64;

Query Match 39.9%; Score 524.5; DB 11; Length 234;
Best Local Similarity 52.0%; Pred. No. 1.2e-36;
Matches 116; Conservative 12; Mismatches 44; Indels 51; Gaps 4;
QY 1 DIQWTTSSLSASLGRVTVCRAQDINRYLNWYQKPDGTVKPLIYTTSLRLLPGVPS 60
DB 21 DIQWTTSSLSASLGRVTVCRAQDINRYLNWYQKPDGTVKPLIYTTSLRLLPGVPS 80
QY 61 RFGSGSGTDYSLTINLEQEDIGTVFCQGNTPPMTFGGTYKLEIKRGSGSGDGGSGG 120
DB 81 RFGSGSGTDYSLTINLEQEDIGTVFCQGNTPPMTFGGTYKLEIKRGSGSGDGGSGG 128
QY 121 GGGGGGSEVQLQSGPGLVFKPGASVKISKDSGYAFNSMNMVVKQRPQGGLWIGRIY 180
DB 129 --ADAAFTVSIFFPSSEQLTSGASV-----VCFLNNFY 160

QY 181 PG-----DGSNYNGKFKGKAILTADKSSSTAYMQLSLT 215
DB 161 PKDINVKNKIDGERONGVLNS---WTDQDSKDSYMSSTLT 200
RESULT 3
Q9D9B8 PRELIMINARY; PRT; 111 AA.
ID Q9D9B8
AC Q9D9B8
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Adult male testis cDNA, RIKEN full-length enriched library,
clone:1700110L11, full insert sequence.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RC MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Komno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schiraldi L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barah G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seva T., Shibata Y., Storch K.-F.,
RA Suzuki H., Ioyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilmig L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kontecki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection."
RL Nature 409:685-690(2001).
DR EMBL; AK007163; BAB24877.1; -.
DR HSSP; P01810; 2FEJ
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Ig; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
SQ SEQUENCE 111 AA; 11976 MW; 874DDF7BD98BD7B2 CRC64;

Query Match 36.9%; Score 486; DB 11; Length 111;
Best Local Similarity 90.2%; Pred. No. 8.4e-34;
Matches 92; Conservative 5; Mismatches 5; Indels 0; Gaps 0;
QY 125 GGGSEVQLQSGPGLVFKPGASVKISKDSGYAFNSMNMVVKQRPQGGLWIGRIYFGDG 184
DB 3 GVHSQVLQSGPGLVFKPGASVKISKDSGYAFNSMNMVVKQRPQGGLWIGRIYFGDG 62
QY 185 DSNYNGKFKGKAILTADKSSSTAYMQLSLTSDSAVFCAR 226
DB 63 DTNYNGKFKGKATLTADKSSSTAYMQLSLTSDSAVFCAR 104

RESULT 4
Q9JL83 PRELIMINARY; PRT; 110 AA.
ID Q9JL83
AC Q9JL83
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Anti-myosin immunoglobulin heavy chain variable region
(Fragment).

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OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALE/c;
RX MEDLINE=20448942; PubMed=1092488;
RA Malkiel S., Liao L., Cunningham M.W., Diamond B.,
RT "T-Cell-dependent antibody response to the dominant epitope of
RT streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive
RT with cardiac myosin.";
RL Infect. Immun. 68:5803-5808 (2000).
DR EMBL; AF206023; AAF69321.1; -.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IgV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 110
SQ SEQUENCE 110 AA; 12052 MW; 8456F2AD219AF95E CRC64;

Query Match 36.7%; Score 483.5; DB 11; Length 110;
Best Local Similarity 83.9%; Pred. No. 1.4e-33;
Matches 94; Conservative 7; Mismatches 8; Indels 3; Gaps 2;

QY 137 PELVPGASVKISKDSGYAFNSMWNWVKQPGGLEWIGRIYPGDSDNYNGKFEKGA 196
Db 1 PELVPGASVKISKASGYTFNSMWNWVKLRPGQGLEWIGRIYPGDSDNYNGKFEKGA 60

QY 197 ILTADKSSSTAYMQLSSLTSDVSAVFCARSGL-LRYANDYMGQGTSTVSS 247
Db 61 TLTADKSSSTAYMQLSSLTSDVSAVFCARSNDVRA--YWGQTLTVTVA 110

RESULT 5
Q8R3H6 PRELIMINARY; PRT; 474 AA.
AC Q8R3H6;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
GN AU044919.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC Strausberg R.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC025447; AAH25447.1; -.
DR MGD; MGI:2144967; AU044919.
DR GO; GO:0005489; P:electron transporter activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR00345; Cyt_c_heme_BS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_3.
DR SMART; SM00406; IgV; 1.
DR PROSITE; PS00190; CYTOCHROME C; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 474 AA; 51748 MW; 8608B57C6CD2874A CRC64;

Query Match 36.3%; Score 478; DB 11; Length 474;
Best Local Similarity 74.0%; Pred. No. 2.5e-32;
Matches 91; Conservative 14; Mismatches 18; Indels 0; Gaps 0;

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QY 125 GGSSEVOIQSQPELVKPGASVKISKDSGYAFNSMWNWVKQPGGLEWIGRIYPGDG 184
Db 16 GVHSQVQLQLQSGPELVKPGASVKISCRASGYAFNSMWNWVKRPRGKLEWIGRIYPGDG 75

QY 185 DSNYNGKFEKAILTADKSSSTAYMQLSSLTSDVSAVFCARSGLLRVANDYMGQGTSTV 244
Db 76 DTHYSGKFGKAKLTADKSSVTAFQLTSLTSDVSAVFCARSGLLRVANDYMGQGTATV 135

QY 245 VSS 247
Db 136 VSS 138

RESULT 6
Q91WS9 PRELIMINARY; PRT; 233 AA.
AC Q91WS9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC Strausberg R.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC013496; AAH13496.1; -.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_2.
DR SMART; SM00406; IgV; 1.
DR PROSITE; PS00835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 233 AA; 25781 MW; B1C184DA149A16EB CRC64;

Query Match 36.3%; Score 477.5; DB 11; Length 233;
Best Local Similarity 48.9%; Pred. No. 1.1e-32;
Matches 109; Conservative 11; Mismatches 52; Indels 51; Gaps 4;

QY 1 DIQMTQTSSLSASLGDRTVTSRASQDIRVNLWYQKPGDTVKFLTYTSRLLPVPS 60
Db 20 DIQMTQTSSLSASLGDRTVTSRASQDIRVNLWYQKPGDTVKFLTYTSRLLPVPS 79

QY 61 RFGSGSGTDYSLTINLEQRIQYFCQGNTPPWTFGGTKLEIKRGGSGSGSGG 120
Db 80 RFGSGSGTDYSLTINLEQRIQYFCQGNTPPWTFGGTKLEIKRGGSGSGSGG 127

QY 121 GSGSGSGSVQLQSQPELVKPGASVKISKDSGYAFNSMWNWVKQPGGLEWIGRIY 180
Db 128 --ADAAPTYSIFPPSSEQLTSGASV-----VCFLNNFY 159

QY 181 PG-----DGSNNGKFEKAILTADKSSSTAYMQLSSLT 215
Db 160 PKDINVKWKIDGSRQNGVLNS---WTDQDSKDSYMSSTLT 199

RESULT 7
Q924Q1 PRELIMINARY; PRT; 142 AA.
AC Q924Q1;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE V23-D-J-C mu protein (Fragment).
GN V23-D-J-C MU.

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OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RA Kozono Y., Kozono H., Azuma T.;
RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
RT Affinity Maturation of B Cell Antigen Receptors in Response to (4-
RT Hydroxy-3-Nitrophenyl)Acetyl (NP).";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB069913; BAB63929.1; -.
DR PIR; F33932; F33932.
DR PIR; I28833; I28833.
DR PIR; PH1156; PH1156.
DR PIR; PH1158; PH1158.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS50835; IG LIKE; 1.
FT NON_TER 1
FT NON_TER 142
SQ SEQUENCE 142 AA; 15622 MW; 24A265CE4EA4318B CRC64;

Query Match 35.7%; Score 471; DB 11; Length 142;
Best Local Similarity 77.3%; Pred. No. 2.2e-32;
Matches 92; Conservative 7; Mismatches 18; Indels 2; Gaps 1;

QY 129 EVQLQSGPELVKPGASVKISCKDGYAFNSWMWVKQRPQGGLWIGRIYPGDGSNY 188
Db 1 QVQLQPGALVKPGASVKLSCKASGYTFTSYMHVWVKQRPQGGLWIGRIYPGDGSNY 60

QY 189 NGKFEKAILTADKSSSTAYMQLSLTSVDSAVYFCARSGLLRYANDYWGQTSVTYSS 247
Db 61 NERFKSKATITVDKSSSTAYMQLSLTSVDSAVYFCARSG--EANDYWGQTSVTYSS 117

RESULT 8
Q91WT1 PRELIMINARY; PRT; 481 AA.
ID Q91WT1
AC Q91WT1;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC Tissue-Colon;
RA Strausberg R.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC013490; AAH13490.1; -.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 4.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS50835; IG LIKE; 4.
DR PROSITE; PS0290; IG_MHC; 2.
KW Hypothetical protein.
SQ SEQUENCE 481 AA; 52105 MW; 97DF68D159463F65 CRC64;

Query Match 35.7%; Score 470; DB 11; Length 481;
Best Local Similarity 73.0%; Pred. No. 1.2e-31;
Matches 92; Conservative 11; Mismatches 21; Indels 2; Gaps 1;

QY 122 GSGGGSEVQLQSGPELVKPGASVKISCKDGYAFNSWMWVKQRPQGGLWIGRIY 181

Db 13 GTAGVQCQVQLQSGPELVKPGASVKISCKASGYTFTSYIHWVKQRPQGGLWIGWIYP 72
QY 182 GGDGSDNYKFEKAILTADKSSSTAYMQLSLTSVDSAVYFCARSGLLRYANDYWGQGT 241
Db 73 GGDGNTKYNKFKGKTLTADKSSSTAYMQLSLTSVDSAVYFCARSG--GWAFDYWGQGT 130
QY 242 SVTVSS 247
Db 131 TLTVSS 136

RESULT 9
Q924Q6 PRELIMINARY; PRT; 145 AA.
ID Q924Q6
AC Q924Q6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE VH186.2-D-J-C mu protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RA Kozono Y., Kozono H., Azuma T.;
RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
RT Affinity Maturation of B Cell Antigen Receptors in Response to (4-
RT Hydroxy-3-Nitrophenyl)Acetyl (NP).";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB067794; BAB63279.1; -.
DR PIR; F28833; F28833.
DR PIR; F33932; F33932.
DR PIR; PH1105; PH1105.
DR PIR; PH1108; PH1108.
DR PIR; PH1114; PH1114.
DR PIR; PH1118; PH1118.
DR PIR; PH1119; PH1119.
DR PIR; PH1125; PH1125.
DR PIR; PH1126; PH1126.
DR PIR; PH1128; PH1128.
DR PIR; PH1129; PH1129.
DR PIR; PH1131; PH1131.
DR PIR; PH1134; PH1134.
DR PIR; PH1137; PH1137.
DR PIR; PH1139; PH1139.
DR PIR; PH1142; PH1142.
DR PIR; PH1144; PH1144.
DR PIR; PH1147; PH1147.
DR PIR; PH1149; PH1149.
DR PIR; PH1150; PH1150.
DR PIR; PH1151; PH1151.
DR PIR; PH1152; PH1152.
DR PIR; PH1153; PH1153.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS50835; IG LIKE; 1.
FT NON_TER 1
FT NON_TER 145
SQ SEQUENCE 145 AA; 16011 MW; 9BC0846D40DF97EA CRC64;

Query Match 35.7%; Score 469.5; DB 11; Length 145;
Best Local Similarity 76.7%; Pred. No. 3e-32;
Matches 92; Conservative 7; Mismatches 20; Indels 1; Gaps 1;

QY 129 EVQLQSGPELVKPGASVKISCKDGYAFNSWMWVKQRPQGGLWIGRIYPGDGSNY 188
Db 1 QVQLQPGALVKPGASVKLSCKASGYTFTSYMHVWVKQRPQGGLWIGRIYDPNSGGTKY 60

QY 189 NGKFEKAILTADKSSSTAYMQLSLTSVDSAVYFCARSGLLRYANDYWGQTSVTYSS 247

[illegible]

OC Mammalia: Eutheria: Rodentia: Sciurognathi: Muridae; Murinae; Mus.

	NCBI_TaxID=10090;
[1]	SEQUENCE FROM N.A.
STRAIN=C57BL/6;	
Kozono Y., Kozono H., Azuma T.;	
"Direct Estimation of Relative Affinity by Flow Cytometry Reveals	
Affinity Maturation of B Cell Antigen Receptors in Response to (4-	
Hydroxy-3-Nitrophenyl)Acetyl (NP).";	
Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.	
EMBL; AB067785; BAB63270.1; -.	
PIR; F28833; F28833.	
PIR; F33932; F33932.	
PIR; P33932; F33932.	
PIR; PH1105; PH1105.	
PIR; PH1108; PH1108.	
PIR; PH1114; PH1114.	
PIR; PH1118; PH1118.	
PIR; PH1119; PH1119.	
PIR; PH1125; PH1125.	
PIR; PH1126; PH1126.	
PIR; PH1128; PH1128.	
PIR; PH1129; PH1129.	
PIR; PH1131; PH1131.	
PIR; PH1134; PH1134.	
PIR; PH1137; PH1137.	
PIR; PH1139; PH1139.	
PIR; PH1142; PH1142.	
PIR; PH1144; PH1144.	
PIR; PH1147; PH1147.	
PIR; PH1149; PH1149.	
PIR; PH1150; PH1150.	
PIR; PH1151; PH1151.	
PIR; PH1152; PH1152.	
PIR; PH1153; PH1153.	
InterPro; IPR007110; Ig-like.	
InterPro; IPR003596; Ig_v.	
Pfam; PF000047; Ig; 1.	
SMART; SM00406; IGv; 1.	
PROSITE; PSS0835; IG_LIKE; 1.	
NON TER	
FT FT	145
NON TER	145
SEQUENCE	145 AA; 16081 MW; ECDBIAl3SE05B8AA CRC64;

	Query Match	35.3%;	Score 464.5;	DB 11;	Length 145;
	Best Local Similarity	75.8%;	Pred. No. 7.9e-32;		
	Matches 91;	Conservative	7;	Mismatches 21;	Indels 1; Gaps 1;
Qy	129	EVQLQQSGPELVKPGASVKISCKDQSGYAFINSWNVWVKRPPQGLEWIGRIYPCGDSDNY	188		
Db	1	QVQLQQPGAEVLKPGASVKISCKASGTYFTSYVHWVKRPPGLEWIGRIDPMSGGTKY	60		
Qy	189	NGKEFGKAILTADSSSTAYVWQLASLSITSVDNAVYFCARSGI-LRYAYMDYWGQGSVTIVSS	247		
Db	61	NEKFKSRATLVKDPKPSSTAYVWQLSLSITSVDNAVYFCARSDYDYDYAYMDYWGQGSVTIVSS	120		

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RESULT 13
Q9Z1C4
ID ID PRELIMINARY; PRT; 118 AA.
AC Q9Z1C4;
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Anti-porcine VCAM map 3F4 heavy chain variable region (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RC SEQUENCE FROM N.A.
RC STRAIN=Balb/c;
RA Mueller J.P., Giannoni M.A., Hartman S.L., Elliott E.A., Squinto S.P.,
RA Matlis L.M., Evans M.J.;

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RT "Humanized porcine VCAM-specific monoclonal antibodies with chimeric
RT IG/G4 constant regions block human leukocyte binding to porcine
RT endothelial cells.";
RRL Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
DR EMBL; U78801; AAD00293.1; -.
DR HSP; P01810; 2EBJ.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 118
FT SEQUENCE 118 AA; 13036 MW; 90HEC559D31EC4FC CRC64;
Query Match 35.2%; Score 463.5; DB 11; Length 118;
Best Local Similarity 74.8%; Pred. No. 7.4e-32;
Matches 89; Conservative 10; Mismatches 19; Indels 1; Gaps 1;
QY 129 EVQLQQSGPELVKPGASVKISCKDSGYAFNFSMMNWVKORPGQGLEWIGRIYPGDDSNY 188
Db 1 QVQVQSGLAEAPPWASVKLSCKASGYNFNSYMWQVKKORPGQGLEWIGAIYPGDGTSY 60
QY 189 NGKFEGKAILTADKSSTAYMQLSSLTSDVSATVFCAKSGLLRYANDYNGQTSTVTSS 247
Db 61 TQFRKGATLTADKSSTAYMQLSSLASEDSAVYYCARRTVGYG-FDYWGQGTTLTVSS 118

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RESULT	14
Q924Q3	PRELIMINARY; PRT; 146 AA.
ID	Q924Q3;
AC	Q924Q3;
DT	01-DEC-2001 (TrEMBLrel. 19, Created)
DT	01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DS	VIL86_2-D-J-C mu protein (Fragment).
OS	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus;
OX	NCBI_TaxID=10096;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=CS7BL/6;
RA	Kozono Y., Kozono H., Azuma T.;
FT	"Direct Estimation of Relative Affinity by Flow Cytometry Reveals
FT	Affinity Maturation of B Cell Antigen Receptors in Response to (4-
FT	Hydroxy-3-Nitrophenyl)Acetyl (NP).";
RL	Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR	EMBL; AB067797, BAB63282.1; -
DR	PIR; F28833; F28833.
DR	PIR; F33932; F33932.
DR	PIR; PH1105; PH1105.
DR	PIR; PH1108; PH1108.
DR	PIR; PH1114; PH1114.
DR	PIR; PH1118; PH1118.
DR	PIR; PH1119; PH1119.
DR	PIR; PH1125; PH1125.
DR	PIR; PH1126; PH1126.
DR	PIR; PH1128; PH1128.
DR	PIR; PH1129; PH1129.
DR	PIR; PH1131; PH1131.
DR	PIR; PH1134; PH1134.
DR	PIR; PH1137; PH1137.
DR	PIR; PH1139; PH1139.
DR	PIR; PH1142; PH1142.
DR	PIR; PH1144; PH1144.
DR	PIR; PH1147; PH1147.
DR	PIR; PH1149; PH1149.
DR	PIR; PH1150; PH1150.
DR	PIR; PH1151; PH1151.
DR	PIR; PH1152; PH1152.
DR	PIR; PH1153; PH1153.
DR	InterPro; IPR007110; Ig-like.

[illegible]

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OM protein - protein search, using sw model

Run on: April 22, 2004, 11:51:48 ; Search time 14 Seconds
(without alignments)
1697.093 Million cell updates/sec

Title: US-10-620-049-25

Perfect score: 1316

Sequence: 1 DIQMTQTSSLSASLGDRVT.....GLLRYMDYMGQGTSTVSS 247

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 78:**

1: Pir1:**

2: Pir2:**

3: Pir3:**

4: Pir4:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	635.5	48.3	287	PC4402	peB leader/Ig hea
2	542.5	41.2	119	A24672	Ig heavy chain pre
3	527.5	40.1	117	PL0237	Ig heavy chain V r
4	526	40.0	108	S69300	Ig kappa chain (cl
5	526	40.0	118	PL0231	Ig heavy chain V r
6	524.5	39.9	117	PL0235	Ig heavy chain V r
7	523	39.7	109	PH0888	Ig kappa chain V r
8	522	39.7	122	A29380	Ig kappa chain pre
9	517	39.3	108	S69303	Ig kappa chain (cl
10	517	39.3	115	PL0238	Ig kappa chain pre
11	516.5	39.2	108	S38862	Ig kappa chain V r
12	515.5	39.2	117	PL0234	Ig heavy chain V r
13	515	39.1	126	A34904	Ig kappa chain pre
14	513	39.0	108	B26405	Ig kappa chain V r
15	509.5	38.7	115	PL0238	Ig heavy chain V r
16	508.5	38.6	107	S69301	Ig kappa chain (cl
17	508	38.6	108	KWMSAR	Ig kappa chain V r
18	508	38.6	108	C26405	Ig kappa chain V r
19	507	38.5	128	A26406	Ig kappa chain V r
20	505	38.4	108	S19370	Ig kappa chain V r
21	505	38.4	108	S69302	Ig kappa chain (cl
22	502	38.1	107	B28044	Ig kappa chain V r
23	502	38.1	107	A28044	Ig kappa chain V r
24	500	38.0	108	PL0282	Ig kappa chain V r
25	500	38.0	127	PH1224	Ig kappa chain pre
26	495.5	37.7	107	S69306	Ig kappa chain (cl
27	488	37.1	112	PL0232	Ig heavy chain V r
28	486	36.9	138	E32513	Ig heavy chain pre
29	485	36.9	107	S32188	Ig kappa chain V r

30 485 36.9 108 2 S11124 Ig kappa chain V r
31 483.5 36.7 140 2 S09216 Ig heavy chain pre
32 482 36.6 246 2 S28950 Ig gamma chain - m
33 482 36.6 446 2 S40295 Ig gamma-2a chain
34 480 36.5 107 2 D48677 Ig kappa chain V-J
35 478 36.3 107 2 B49026 Ig kappa chain V r
36 477 36.2 105 2 PH0087 Ig kappa chain V r
37 477 36.2 111 2 A38740 Ig kappa chain V r
38 475 36.1 109 2 PL0233 Ig heavy chain V r
39 474 36.0 108 2 B30551 Ig kappa chain V r
40 467 35.5 111 2 E38740 Ig kappa chain V r
41 467 35.5 111 2 C38740 Ig kappa chain V r
42 466 35.4 111 2 C38740 Ig kappa chain V r
43 465 35.4 138 2 S21810 Ig heavy chain V r
44 465.5 35.4 120 2 PD0008 Ig heavy chain V r
45 464.5 35.3 120 2 B22769 Ig heavy chain V r

ALIGNMENTS

RESULT 1

PC4402

peB leader/Ig heavy chain anti-NP/linker type 205/alkaline phosphatase fusion protein
C;Species: synthetic
C;Date: 06-Nov-1998 #sequence_revision 06-Nov-1998 #text_change 06-Nov-1998
C;Accession: PC4402

R;Suzuki, C.; Ueda, H.; Suzuki, E.; Nagamune, T.
J. Biochem. 122, 322-329, 1997

A;Title: Construction, bacterial expression, and characterization of hapten-specific si

A;Reference number: PC4402

A;Accession: PC4402

A;Molecule type: DNA

A;Residues: 1-287 <SUZ>

C;Keywords: fusion protein

Query Match 48.3%; Score 635.5; DB 4; Length 287;

Best Local Similarity 53.3%; Pred. No. 36;

Matches 138; Conservative 24; Mismatches 82; Indels 15; Gaps 5;

Qy 1 DIQMTQT-TSSLSASLGDRVTVSSCRASQ---DIRNLYNWYQCKPDGTVKFLIYVTSRLLP 56

Db 24 DIQAVVVTQESALTTPGETVTLTCRSSTGAVTTSYANWVQEKPDHLPGLTIGGTNNRAP 83

Qy 57 GVPSPFGSGSGTDSLTLNNLEQEDIGTYFCQCGNTPTPTFGGCTKLEI-----KRG 109

Db 84 GVPARESGSLIGDKAALITGTAQTEDEALFYCALWYNHNVFVGCTKLTVLSSADDAKDD 143

Qy 110 GGGSDCGSGSGSGSGGSEVLOQSGPELVKPGASVKISCKDSGYAFNSSWNVKQRP 169

Db 144 DAKDDAKDDAKDDAKDQ---QVQLQOPGAEVLKPGASVKLSCKASGYTFTSYMHWKQRP 200

Qy 170 GQGLEWIGRIYPGDGDPSNNGKFEKAILTADKSSSTAYMQLSSLTSDSAVYFCARSGL 229

Db 201 GRGLEWIGRIDPSNGGTYKNEKFKSKATLTVDKPSSTAYMQLSSLTSDSAVYCARVDY 260

Qy 230 LRYA-MDYNGQGTSTVSS 247

Db 261 YGSSYFDYMGQGTTLTVSS 279

RESULT 2

A24672

Ig heavy chain precursor V region (VIMU-3.2) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 23-Jul-1999

C;Accession: A24672

R;Winter, E.; Radbruch, A.; Krawinkel, U.

EMBO J. 4, 2861-2867, 1985

A;Reference number: A91022; PMID:86055722; PMID:2998759

A;Accession: A24672

A;Molecule type: DNA

A;Residues: 1-119 <WIN>

A;Cross-references: GB:X03088; NID:G52378; PIDN:CAA26881.1; PID:G773578
A;Note: This sequence was determined from the germline gene
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; chain V region VMO-3.2 #status predicted <MAT>
F;18-101/Domain: immunoglobulin homology <IMM>

Query Match 41.2%; Score 542.5; DB 2; Length 119;
Best Local Similarity 85.5%; Pred. No. 2.6e-30;
Matches 103; Conservative 7; Mismatches 7; Indels 3; Gaps 1;

QY 128 SEVQLQDSGPPELVKPGASVKISCKDQSGYAFNSWNNWVKQRPQGQLEWIGRIYFGDGSNY 187
DB 3 SQVQLQDSGPPELVKPGASVKISCKASGYAFSSWNNWVKQRPQGLEWIGRIYFGDGSNT 62

QY 188 YNGKPEGKATLTADKSSSTAYNQLSSTSDSAVFCARSLRLRYAMDYWGQGTSTVTS 247
DB 63 YNGKFKGKATLTADKSSSTAYNQLSSTSDSAVFCARD---YWGSDYWGQGTSTVTS 119

RESULT 3
P;10237
Ig heavy chain V region (anti-DNA, 1A11VH) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 16-Aug-1996
C;Accession: PLO237
R;Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A.
J. Exp. Med. 171, 265-297, 1990
A;Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic
A;Reference number: PLO231; MUID:90111618; PMID:2104919
A;Accession: PLO237
A;Molecule type: mRNA
A;Residues: 1-117 <SHL>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-30/Region: framework 1
F;31-35/Region: complementarity-determining 1
F;36-49/Region: complementarity-determining 2
F;50-66/Region: complementarity-determining 3
F;67-98/Region: framework 3
F;99-109/Region: complementarity-determining 3
F;110-117/Region: framework 4

Query Match 40.1%; Score 527.5; DB 2; Length 117;
Best Local Similarity 85.5%; Pred. No. 2.6e-29;
Matches 100; Conservative 6; Mismatches 10; Indels 1; Gaps 1;

QY 129 EVQLQDSGPPELVKPGASVKISCKDQSGYAFNSWNNWVKQRPQGQLEWIGRIYFGDGSNY 188
DB 1 QVQLQDSGPPELVKPGGSKISCKASGYAFSSWNNWVKQRPQGLEWIGRIYFGDGSNTY 60

QY 189 NGKPEGKATLTADKSSSTAYNQLSSTSDSAVFCARS-GLRLRYAMDYWGQGTSTV 244
DB 61 NGKFKGKATLTADKSSSTAYNQLSSTSDSAVFCARSKYSYVMDYWGQGTSTV 117

RESULT 4
S69900
Ig kappa chain (clone KL2.18 / KL4B10 / KL4C11) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 21-Jan-2000
C;Accession: S69900; S69907; S69908
R;Wysocki, L.J.; Creadon, G.; Lehmann, K.R.; Cambier, J.C.
Immunology 75, 116-121, 1992
A;Title: B-cell proliferation initiated by Ia cross-linking and sustained by interleukin
A;Reference number: S69900; MUID:92165291; PMID:1537587
A;Accession: S69900
A;Status: preliminary; translation not shown
A;Molecule type: DNA
A;Residues: 1-108 <WYS>
A;Cross-references: EMBL:X55041; NID:G511023; PIDN:CAA38881.1; PID:G511024
A;Accession: S69907

A;Status: preliminary; translation not shown
A;Molecule type: DNA
A;Residues: 1-108 <WY2>
A;Cross-references: EMBL:X55048; NID:G511037; PIDN:CAA38888.1; PID:G511038
A;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; chain V region VMO-3.2 #status predicted <MAT>
F;18-101/Domain: immunoglobulin homology <IMM>

Query Match 40.0%; Score 526; DB 2; Length 108;
Best Local Similarity 92.8%; Pred. No. 3e-29;
Matches 100; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 DIQWTTTSLASLSDRVTVSCRASQDIRNYLNWVQKPDGTVKPLIYTSLLFCVPS 60
DB 1 DIQWTTTSLASLSDRVTVISCRASQDISNYLNWVQKPDGTVKPLIYTSLLHSGVPS 60

QY 61 RFGSGSGTDYSLTINNLEQEDIGTVFCQGNTPPWTFGGGTGLEIKR 108
DB 61 RFGSGSGTDYSLTINNLEQEDIGTVFCQGNTPPWTFGGGTGLEIKR 108

RESULT 5

P;10231
Ig heavy chain V region (anti-DNA, D20VH) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 16-Aug-1996
C;Accession: PLO231
R;Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A.
J. Exp. Med. 171, 265-297, 1990
A;Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic
A;Reference number: PLO231; MUID:90111618; PMID:2104919
A;Accession: PLO231
A;Molecule type: mRNA
A;Residues: 1-118 <SHL>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-30/Region: framework 1
F;31-35/Region: complementarity-determining 1
F;36-49/Region: complementarity-determining 2
F;50-66/Region: complementarity-determining 3
F;67-98/Region: framework 3
F;99-110/Region: complementarity-determining 3
F;111-118/Region: framework 4

Query Match 40.0%; Score 526; DB 2; Length 118;
Best Local Similarity 84.7%; Pred. No. 3.3e-29;
Matches 100; Conservative 7; Mismatches 9; Indels 2; Gaps 1;

QY 129 EVQLQDSGPPELVKPGASVKISCKDQSGYAFNSWNNWVKQRPQGQLEWIGRIYFGDGSNY 188
DB 1 QVQLQDSGPPELVKPGGSKISCKASGYAFSSWNNWVKQRPQGLEWIGRIYFGDGSNTY 60

QY 189 NGKPEGKATLTADKSSSTAYNQLSSTSDSAVFCARSLRLRYAMD---YWGQGTSTV 244
DB 61 NGKFKGKATLTADKSSSTAYNQLSSTSDSAVFCARSLRLRYAMDYWGQGTSTV 118

RESULT 6

P;10235
Ig heavy chain V region (anti-DNA, 2F2VH and 4H8VH) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 16-Aug-1996
C;Accession: PLO235
R;Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A.
J. Exp. Med. 171, 265-297, 1990
A;Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic
A;Reference number: PLO231; MUID:90111618; PMID:2104919
A;Accession: PLO235

A:Molecule type: mRNA
A:Residues: 1-117 <SHL>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-30/Region: framework 1
F:15-98/Domain: immunoglobulin homology <IMM>
F:31-35/Region: complementarity-determining 1
F:36-45/Region: framework 2
F:50-65/Region: complementarity-determining 2
F:67-98/Region: framework 3
F:99-109/Region: complementarity-determining 3
F:110-117/Region: framework 4

Query Match 39.9%; Score 524.5; DB 2; Length 117;
Best Local Similarity 84.6%; Pred. No. 4.2e-29;
Matches 99; Conservative 7; Mismatches 10; Indels 1; Gaps 1;

QY 129 EVLOQSGPGLYKPGASVKISCKDGYAFNSWVWVQKPGGLEWIGRIYFGDGSDNY 188
DB 1 QVLOQSGPGLYKPGASVKISCKDGYAFNSWVWVQKPGGLEWIGRIYFGDGSDNY 60

QY 189 NGKFEKALITADKSSSTAYMQLSSLTSDSAVYFCARSKYSYVLDYWGQGTST 244
DB 61 NGKFEKALITADKSSSTAYMQLSSLTSDSAVYFCARSKYSYVLDYWGQGTST 117

RESULT 7
PH0888
Ig kappa chain V region (anti-CD3) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 21-Jan-2000
C:Accession: PH0888
R:Shalaby, M.R.; Shepard, H.M.; Presta, L.; Rodriguez, M.L.; Beverley, P.C.L.; Feldmann, J. Exp. Med. 175, 217-225, 1992
A:Title: Development of humanized bispecific antibodies reactive with cytotoxic lymphocytes
A:Reference number: PH0885; MUID:92113462; PMID:1346155
A:Accession: PH0888
A:Molecule type: mRNA
A:Residues: 1-109 <SHA>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 39.7%; Score 523; DB 2; Length 109;
Best Local Similarity 91.7%; Pred. No. 4.9e-29;
Matches 99; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 DIQMTQTSSLSASLGDRVTVCRAQDINRYLNWYQKPDGTGKFLIYTSRLPGVPS 60
DB 1 DIQMTQTSSLSASLGDRVTVCRAQDINRYLNWYQKPDGTGKFLIYTSRLPGVPS 60

QY 61 RFGSGSGTDYSLTINLEQEDIGTYFCQQGNTLPWTFGGGKLEIKR 108
DB 61 RFGSGSGTDYSLTINLEQEDIGTYFCQQGNTLPWTFGGGKLEIKR 108

RESULT 8
A29380
Ig kappa chain precursor V region (AC-1001) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 21-Jan-2000
C:Accession: A29380
R:Chen, H.T.; Kabat, E.A.; Lundblad, A.; Ratcliffe, R.M. J. Biol. Chem. 262, 13579-13583, 1987
A:Title: Nucleotide and translated amino acid sequences of cDNA coding for the variable
A:Reference number: A92612; MUID:88007582; PMID:3115981
A:Accession: A29380
A:Molecule type: mRNA
A:Residues: 1-122 <CHE>
A:Cross-references: GB:M17160; GB:J02815; NID:g196895; PIDN:AAA38824.1; PID:g196896
A:Note: the authors translated the codon TTC for residue 1 as Leu
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

F:30-104/Domain: immunoglobulin homology <IMM>

Query Match 39.7%; Score 522; DB 2; Length 122;
Best Local Similarity 91.7%; Pred. No. 6.4e-29;
Matches 99; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 DIQMTQTSSLSASLGDRVTVCRAQDINRYLNWYQKPDGTGKFLIYTSRLPGVPS 60
DB 15 DIQMTQTSSLSASLGDRVTVCRAQDINRYLNWYQKPDGTGKFLIYTSRLPGVPS 74

QY 61 RFGSGSGTDYSLTINLEQEDIGTYFCQQGNTLPWTFGGGKLEIKR 108
DB 75 RFGSGSGTDYSLTINLEQEDIGTYFCQQGNTLPWTFGGGKLEIKR 122

RESULT 9
S69903
Ig kappa chain (clone KL2.29 / KL2.33 / KL3.8) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 21-Jan-2000
C:Accession: S69903; S69904; S69905
R:Wysocki, L.J.; Creadon, G.; Lehmann, K.R.; Cambier, J.C. Immunology 75, 116-121, 1992
A:Title: B-cell proliferation initiated by Ia cross-linking and sustained by interleukin
A:Reference number: S69900; MUID:92165291; PMID:1537587
A:Accession: S69903
A:Status: preliminary; translation not shown
A:Molecule type: DNA
A:Residues: 1-108 <WYS>
A:Cross-references: EMBL:X55044; NID:g511029; PIDN:CAA38884.1; PID:g511030
A:Accession: S69904
A:Status: preliminary; translation not shown
A:Molecule type: DNA
A:Residues: 1-108 <WY2>
A:Cross-references: EMBL:X55045; NID:g511031; PIDN:CAA38885.1; PID:g511032
A:Accession: S69905
A:Status: preliminary; translation not shown
A:Molecule type: DNA
A:Residues: 1-108 <WY3>
A:Cross-references: EMBL:X55046; NID:g511033; PIDN:CAA38886.1; PID:g511034
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 39.3%; Score 517; DB 2; Length 108;
Best Local Similarity 91.7%; Pred. No. 1.2e-28;
Matches 99; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 DIQMTQTSSLSASLGDRVTVCRAQDINRYLNWYQKPDGTGKFLIYTSRLPGVPS 60
DB 1 DIQMTQTSSLSASLGDRVTVCRAQDINRYLNWYQKPDGTGKFLIYTSRLPGVPS 60

QY 61 RFGSGSGTDYSLTINLEQEDIGTYFCQQGNTLPWTFGGGKLEIKR 108
DB 61 RFGSGSGTDYSLTINLEQEDIGTYFCQQGNTLPWTFGGGKLEIKR 108

RESULT 10
JL0080
Ig kappa chain precursor V region (anti-phenyloxazolone, 18C10) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 21-Jan-2000
C:Accession: JL0080
R:Kaartinen, M.; Rocca-Serra, J.; Maekela, O. Mol. Immunol. 25, 859-865, 1988
A:Title: Combinatorial association of V genes: one VH gene codes for three non-cross-re
A:Reference number: JL0076; MUID:89096973; PMID:3211160
A:Accession: JL0080
A:Molecule type: mRNA
A:Residues: 1-115 <XAA>
A:Cross-references: GB:M27793; NID:g197161; PIDN:AAA38937.1; PID:g197162
A:Note: the authors translated the codon AGG for residue 30 as Ser
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin

F:1-6/Domain: signal sequence (fragment) #status predicted <SIG>
F:7-115/Product: Ig light chain #status predicted <NAR>
F:22-96/Domain: immunoglobulin homology <IMM>
F:30-40/Region: complementarity-determining 1
F:56-62/Region: complementarity-determining 2

Query Match 39.3%; Score 517; DB 2; Length 115;
Best Local Similarity 91.7%; Pred. No. 1.3e-28;
Matches 99; Conservative 3; Mismatches 6; Indels 0; Gaps 0;
QY 1 DIQMTQTSSLSASLGDRVTVCSCASQDIRNYLNWYQKPDGVTKFLIYTSRLLPVPS 60
DB 7 DIQMTQTSSLSASLGDRVTVCSCASQDIRNYLNWYQKPDGVTKFLIYTSRLHSGVPS 66
QY 61 RFGSGSGTDYSLTINLEQEDIGTYFCQGNTPPWTFGGGKLEIKR 108
DB 67 RFGSGSGTDYSLTINLEQEDIGTYFCQGNTPPWTFGGGKLEIKR 114

RESULT 11

Ig kappa chain V region - mouse
C:Species: Mus musculus (house mouse)
C:Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000
C:Accession: S38862
R:Fischer, R.; Voss, A.; Hunziker, W.; Stierhof, Y.D.; Kreuzaler, F.
submitted to the EMBL Data Library, August 1993
A:Description: Production and cloning of TWV-specific monoclonal antibodies.
A:Reference number: S37200
A:Accession: S38862
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-108 <PIS>
A:Cross-references: EMBL:X75854; NID:G429109; PID:G429110
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 39.2%; Score 516.5; DB 2; Length 108;
Best Local Similarity 90.7%; Pred. No. 1.3e-28;
Matches 98; Conservative 4; Mismatches 5; Indels 1; Gaps 1;
QY 1 DIQMTQTSSLSASLGDRVTVCSCASQDIRNYLNWYQKPDGVTKFLIYTSRLLPVPS 60
DB 1 DVQMTQTSSLSASLGDRVTVCSCASQDIRNYLNWYQKPDGVTKFLIYTSRLHSGVPS 60
QY 61 RFGSGSGTDYSLTINLEQEDIGTYFCQGNTPPWTFGGGKLEIK 107
DB 61 RFGSGSGTDYSLTINLEQEDIGTYFCQGNTPPWTFGGGKLEIK 108

RESULT 12

Ig heavy chain V region (anti-DNA, 3H9VH) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 16-Aug-1996
C:Accession: PLO234
R:Shlomchik, M.; Mascello, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A.
J. Exp. Med. 171, 265-297, 1990
A:Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic
A:Reference number: PLO231; MUID:90111618; PMID:2104919
A:Accession: PLO234
A:Molecule type: mRNA
A:Residues: 1-117 <SHL>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-30/Region: framework 1
F:15-98/Domain: immunoglobulin homology <IMM>
F:31-35/Region: complementarity-determining 1
F:36-49/Region: framework 2
F:50-66/Region: complementarity-determining 2
F:67-98/Region: framework 3
F:99-109/Region: complementarity-determining 3

F:110-117/Region: framework 4

Query Match 39.2%; Score 515.5; DB 2; Length 117;
Best Local Similarity 84.6%; Pred. No. 1.7e-28;
Matches 99; Conservative 5; Mismatches 12; Indels 1; Gaps 1;
QY 129 EYLOQSGPELVKPGASVKISCKDSGYAFNNSMMWVQKPGQGLEWIGRIYPRGDGNY 188
DB 1 QVLOQSGPELVKPGGSKVKISCKVSGYAFSSMMWVQKPGQGLEWIGRIYPRGDGNY 60
QY 189 NGKFEKAITADKSSSTAYMQLSITSDSAVYFCARS-GELRYAMDYWGQGTSTV 244
DB 61 NGKFEKAITADKSSSTAYMQLSITSDSAVYFCARSKYSYVMDYWGQGTSTV 117

RESULT 13

Ig kappa chain precursor V region (5-27) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 27-Jul-1990 #sequence_revision 27-Jul-1990 #text_change 21-Jan-2000
C:Accession: A34904
R:Bedzyk, W.D.; Herron, J.N.; Edmundson, A.B.; Voss Jr., E.W.
J. Biol. Chem. 265, 133-138, 1990
A:Title: Active site structure and antigen binding properties of idiotypically cross-reacting
A:Reference number: A34903; MUID:90094387; PMID:2104617
A:Accession: A34904
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-126 <BED>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:35-109/Domain: immunoglobulin homology <IMM>

Query Match 39.1%; Score 515; DB 2; Length 126;
Best Local Similarity 92.5%; Pred. No. 2e-28;
Matches 98; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
QY 1 DIQMTQTSSLSASLGDRVTVCSCASQDIRNYLNWYQKPDGVTKFLIYTSRLLPVPS 60
DB 20 DIQMTQTSSLSASLGDRVTVCSCASQDIRNYLNWYQKPDGVTKFLIYTSRLHSGVPS 79
QY 61 RFGSGSGTDYSLTINLEQEDIGTYFCQGNTPPWTFGGGKLEI 106
DB 80 RFGSGSGTDYSLTINLEQEDIGTYFCQGNTPPWTFGGGKLEI 125

RESULT 14

Ig kappa chain V region (1F6) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 21-Jan-2000
C:Accession: B26405
R:Smith, J.A.; Margolies, M.N.
Biochemistry 26, 604-612, 1987
A:Title: Complete amino acid sequences of the heavy and light chain variable regions from
A:Reference number: A90518; MUID:87157677; PMID:3103682
A:Accession: B26405
A:Molecule type: protein
A:Residues: 1-108 <SMI>
A:Experimental source: strain A/J
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 39.0%; Score 513; DB 2; Length 108;
Best Local Similarity 91.7%; Pred. No. 2.3e-28;
Matches 99; Conservative 2; Mismatches 7; Indels 0; Gaps 0;
QY 1 DIQMTQTSSLSASLGDRVTVCSCASQDIRNYLNWYQKPDGVTKFLIYTSRLLPVPS 60
DB 1 DIQMTQTSSLSASLGDRVTVCSCASQDIRNYLNWYQKPDGVTKFLIYTSRLHSGVPS 60

QY 61 RFGSGSGTDYSLTINNLEQEDIGTVPCQCGNTPTPTFGGTTKLEIKR 108
 Db 61 RFGSGSGTDYSLTINNLEQEDIGTVPCQCGNTPTPTFGGTTKLEIKR 108

RESULT 15

PL0238
 Ig heavy chain V region (anti-DNA, 6NVH and 6QVH) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 16-Aug-1996
 C:Accession: PL0238
 R:Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A.
 J. Exp. Med. 171, 263-297, 1990
 A:Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic
 A:Reference number: PL0231; MUID:90111618; PMID:2104919
 A:Accession: PL0238
 A:Molecule type: mRNA
 A:Residues: 1-115 <SHL>
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 F:1-30/Region: framework 1
 F:15-98/Domain: immunoglobulin homology <IMM>
 F:31-35/Region: complementarity-determining 1
 F:36-49/Region: framework 2
 F:50-66/Region: complementarity-determining 2
 F:67-98/Region: framework 3
 F:99-107/Region: complementarity-determining 3
 F:108-115/Region: framework 4

Query Match 38.7%; Score 509.5; DB 2; Length 115;
 Best Local Similarity 84.5%; Pred. No. 4.3e-28;
 Matches 98; Conservative 5; Mismatches 12; Indels 1; Gaps 1;

QY 129 EYLOQSGPELYKPGASVKISKDSGYAFNSWMNWKQRPQGLEWIGRIYPGDGSNY 188
 Db 1 QYLOQSGPELYKPGGSVKISKASGYAFSSWMNWKQRPQGLEWIGRIYPGDGSNY 60

QY 189 NGKFEKALTADKSSSTAYMQLSLTSYDSAVYFCARSGLLRYANDYWGQSTVT 244
 Db 61 NGKFRKALTADKSSSTAYMQLSLTSYDSAVYFCARYRL-LPFDYWGQSTVT 115

Search completed: April 22, 2004, 11:57:12
 Job time : 15 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 22, 2004, 11:52:48 ; Search time 16.5 seconds
(without alignments)
772.825 Million cell updates/sec

Title: US-10-620-049-25

Perfect score: 1316
Sequence: 1 DQMTQTSSLSASLGDRVT.....GLRYAMDYWGQTSVTSS 247

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*
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2: /cgn2_6/prodata/2/aa/5B_COMB.pep:*
3: /cgn2_6/prodata/2/aa/6A_COMB.pep:*
4: /cgn2_6/prodata/2/aa/6B_COMB.pep:*
5: /cgn2_6/prodata/2/aa/5CTUS_COMB.pep:*
6: /cgn2_6/prodata/2/aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	952	72.3	302	1	US-08-121-054C-18
2	952	72.3	302	1	US-08-539-436-18
3	952	72.3	302	4	US-09-813-659-18
4	952	72.3	302	4	US-09-549-067A-18
5	951	72.3	274	4	US-09-813-659-30
6	951	72.3	274	4	US-09-549-067A-30
7	951	72.3	302	1	US-08-121-054C-30
8	951	72.3	302	3	US-08-539-436-30
9	951	72.3	302	4	US-09-813-659-32
10	951	72.3	302	4	US-09-549-067A-32
11	819	62.2	271	2	US-08-400-115-4
12	812	61.7	355	3	US-08-875-811-41
13	812	61.7	355	3	US-08-875-811-49
14	812	61.7	355	3	US-08-875-811-64
15	812	61.7	358	3	US-08-875-811-45
16	812	61.7	358	3	US-08-875-811-51
17	812	61.7	360	3	US-08-875-811-47
18	812	61.7	379	3	US-08-875-811-43
19	796.5	60.5	240	1	US-08-488-113B-147
20	796.5	60.5	240	1	US-08-477-484B-147
21	796.5	60.5	240	2	US-08-646-360-147
22	796.5	60.5	240	3	US-08-839-765-147
23	796.5	60.5	240	3	US-09-136-389-147
24	796.5	60.5	240	4	US-09-610-838-147
25	796.5	60.5	240	4	US-09-711-485-147
26	793.5	60.3	301	2	US-08-656-906-25
27	793.5	60.3	301	3	US-09-217-847-25

28	784	59.6	244	1	US-08-230-843-2	Sequence 2, Appli
29	784	59.6	244	2	US-08-636-936-2	Sequence 2, Appli
30	755	57.4	240	3	US-08-392-338A-11	Sequence 11, Appl
31	755	57.4	240	3	US-09-166-750-11	Sequence 11, Appl
32	755	57.4	240	3	US-08-166-093-11	Sequence 11, Appl
33	755	57.4	240	3	US-09-172-019-11	Sequence 11, Appl
34	755	57.4	240	3	US-09-166-094-11	Sequence 11, Appl
35	755	57.4	240	4	US-08-443-213-11	Sequence 11, Appl
36	743	56.5	238	2	US-08-224-591-12	Sequence 12, Appl
37	743	56.5	238	2	US-08-392-338A-21	Sequence 21, Appl
38	743	56.5	238	2	US-08-926-789-12	Sequence 12, Appl
39	743	56.5	238	3	US-09-166-750-21	Sequence 21, Appl
40	743	56.5	238	3	US-09-166-093-21	Sequence 21, Appl
41	743	56.5	238	3	US-09-172-019-21	Sequence 21, Appl
42	743	56.5	238	3	US-09-166-094-21	Sequence 21, Appl
43	743	56.5	238	4	US-09-443-213-21	Sequence 21, Appl
44	743	56.5	239	5	PCT-US93-11138-12	Sequence 12, Appl
45	735	55.9	239	2	US-08-860-174A-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-08-121-054C-18
; Sequence 18, Application US/08121054C
; Patent No. 5637481
; GENERAL INFORMATION:
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Galliland, Lisa K.
; APPLICANT: Hayden, Martha S.
; APPLICANT: Linsley, Peter S.
; APPLICANT: Bajorath, Jürgen
; APPLICANT: Fell, Perry
; TITLE OF INVENTION: Expression Vectors Encoding Bispecific
; TITLE OF INVENTION: Fusion Proteins and Methods of Producing Biologically
; TITLE OF INVENTION: Active Bispecific Fusion Proteins in a Mammalian Cell
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant & Gould
; STREET: 11150 Santa Monica Blvd., Suite 400
; CITY: Los Angeles
; STATE: CA
; COUNTRY: USA
; ZIP: 90025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/121,054C
; FILING DATE: 13-SEP-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/013,420
; FILING DATE: 01-FEB-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Adriano, Sarah B.
; REGISTRATION NUMBER: 34,470
; REFERENCE/DOCKET NUMBER: 30436.18US01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 310-445-1140
; TELEFAX: 310-445-9031
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 302 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-121-054C-18

Query Match 72.3%; Score 952; DB 1; Length 302;

Best Local Similarity 75.8%; Pred. No. 4.1e-67; DB 3; Length 302;
Matches 191; Conservative 14; Mismatches 39; Indels 8; Gaps 3;
QY 1 DIQMTQTSSLSASLGDRVTUSCRASQDIRNYLWYQOKPDGTVKFLIYVTSRLLPGVPS 60
DB 24 DIQMTQTSSLSASLGDRVTUSCRASQDIRNYLWYQOKPDGTVKFLIYVTSRLLPGVPS 83
QY 61 RPSGSGSGTDYSLTINNLEQEDIGTYFCQOQNTPTWTFGGGTGKLEIKRGSGSGDGGSGG 120
DB 84 RPSGSGSGTDYSLTINNLEQEDIGTYFCQOQNTPTWTFGGGTGKLEIKRGSGSGDGGSGG 140
QY 121 GSGGGGGS--EVLOQSGPGLVPGASVKISCKDSGYAFNSWVWVQKPCQGLEWIGR 178
DB 141 GSGGGGGSIDEVLOQSGPGLVPGASVTMSCKASGYSFTGYVNWKLQSHKGNLEWIGL 200
QY 179 IYPGDSNNGKFEKAILTADKSSSTAYMOLSLTSDSAVYFCARSGLL---RYAMD 235
DB 201 INPWKGLTYNQKFKGKATLVDKSSSTAYMOLSLTSDSAVYFCARSGLL---RYAMD 260
QY 236 YWQGTSTVTVSS 247
DB 261 VMGAGTCTVSS 272

RESULT 2
US-08-539-436-18
; Sequence 18, Application US/08539436
; Patent No. 6132992
; GENERAL INFORMATION:
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Gilliland, Lisa K.
; APPLICANT: Hayden, Martha S.
; APPLICANT: Linsley, Peter S.
; APPLICANT: Bajorath, Jurgen
; APPLICANT: Fell, Perry
; TITLE OF INVENTION: Expression Vectors Encoding Bispecific
; TITLE OF INVENTION: Fusion Proteins and Methods of Producing Biologically
; TITLE OF INVENTION: Active Bispecific Fusion Proteins in a Mammalian Cell
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant & Gould
; STREET: 11150 Santa Monica Blvd., Suite 400
; CITY: Los Angeles
; STATE: CA
; COUNTRY: USA
; ZIP: 90025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/08/539,436
; FILING DATE: 05-OCT-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/121,054
; FILING DATE: 13-SEP-1993
; APPLICATION NUMBER: US 08/013,420
; FILING DATE: 01-FEB-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Adriano, Sarah B.
; REGISTRATION NUMBER: 34,470
; REFERENCE/DOCKET NUMBER: 30436.18US01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 310-445-1140
; TELEFAX: 310-445-9031
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 302 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear

US-08-539-436-18
Query Match 72.3%; Score 952; DB 3; Length 302;
Best Local Similarity 75.8%; Pred. No. 4.1e-67;
Matches 191; Conservative 14; Mismatches 39; Indels 8; Gaps 3;
QY 1 DIQMTQTSSLSASLGDRVTUSCRASQDIRNYLWYQOKPDGTVKFLIYVTSRLLPGVPS 60
DB 24 DIQMTQTSSLSASLGDRVTUSCRASQDIRNYLWYQOKPDGTVKFLIYVTSRLLPGVPS 83
QY 61 RPSGSGSGTDYSLTINNLEQEDIGTYFCQOQNTPTWTFGGGTGKLEIKRGSGSGDGGSGG 120
DB 84 RPSGSGSGTDYSLTINNLEQEDIGTYFCQOQNTPTWTFGGGTGKLEIKRGSGSGDGGSGG 140
QY 121 GSGGGGGS--EVLOQSGPGLVPGASVKISCKDSGYAFNSWVWVQKPCQGLEWIGR 178
DB 141 GSGGGGGSIDEVLOQSGPGLVPGASVTMSCKASGYSFTGYVNWKLQSHKGNLEWIGL 200
QY 179 IYPGDSNNGKFEKAILTADKSSSTAYMOLSLTSDSAVYFCARSGLL---RYAMD 235
DB 201 INPWKGLTYNQKFKGKATLVDKSSSTAYMOLSLTSDSAVYFCARSGLL---RYAMD 260
QY 236 YWQGTSTVTVSS 247
DB 261 VMGAGTCTVSS 272

RESULT 3
US-09-813-659-18
; Sequence 18, Application US/09813659
; Patent No. 6482919
; GENERAL INFORMATION:
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Hayden, Martha S.
; APPLICANT: Linsley, Peter S.
; APPLICANT: Bajorath, Jurgen
; APPLICANT: Fell, H. Perry
; APPLICANT: Gilliland, Lisa K.
; TITLE OF INVENTION: EXPRESSION VECTORS ENCODING BISPECIFIC FUSION PROTEINS
; TITLE OF INVENTION: AND METHODS OF PRODUCING BIOLOGICALLY ACTIVE BISPECIFIC
; TITLE OF INVENTION: FUSION PROTEINS IN A MAMMALIAN CELL
; FILE REFERENCE: 30436.18USD2
; CURRENT APPLICATION NUMBER: US/09/813,659
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 09/549,067
; PRIOR FILING DATE: 2000-04-13
; PRIOR APPLICATION NUMBER: 08/539,436
; PRIOR FILING DATE: 1995-10-05
; PRIOR APPLICATION NUMBER: 08/121,054
; PRIOR FILING DATE: 1993-09-13
; PRIOR APPLICATION NUMBER: 08/013,420
; PRIOR FILING DATE: 1993-02-01
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 302
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-813-659-18
Query Match 72.3%; Score 952; DB 4; Length 302;
Best Local Similarity 75.8%; Pred. No. 4.1e-67;
Matches 191; Conservative 14; Mismatches 39; Indels 8; Gaps 3;
QY 1 DIQMTQTSSLSASLGDRVTUSCRASQDIRNYLWYQOKPDGTVKFLIYVTSRLLPGVPS 60
DB 24 DIQMTQTSSLSASLGDRVTUSCRASQDIRNYLWYQOKPDGTVKFLIYVTSRLLPGVPS 83
QY 61 RPSGSGSGTDYSLTINNLEQEDIGTYFCQOQNTPTWTFGGGTGKLEIKRGSGSGDGGSGG 120
DB 84 RPSGSGSGTDYSLTINNLEQEDIGTYFCQOQNTPTWTFGGGTGKLEIKRGSGSGDGGSGG 140
QY 121 GSGGGGGS--EVLOQSGPGLVPGASVKISCKDSGYAFNSWVWVQKPCQGLEWIGR 178

Db 141 GSGGGGSDIDEVQOQSGPELVKPGASMTWSCASGYSTGYIVNWLKQSHGNLEWIGL 200
Qy 179 IYPGDSNNGKFEKGKAILTADKSSSTAYMQLSSLTSDSVAVYFCARSGLL---RYAMD 235
Db 201 INPKGLTTYNQKFKGKATLTVDKSSSTAYMQLSSLTSDSVAVYFCARSGYGSDWYFD 260
Qy 236 YWGQTSVTVSS 247
Db 261 VWGAGTCTVSS 272

RESULT 4
US-09-549-067A-18
; Sequence 18, Application US/09549067A
; Patent No. 6623940
; GENERAL INFORMATION:
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Hayden, Martha S.
; APPLICANT: Linsley, Peter S.
; APPLICANT: Bajorath, Jurgen
; APPLICANT: Fell, H. Perry
; APPLICANT: Gilliland, Lisa K.
; TITLE OF INVENTION: EXPRESSION VECTORS ENCODING BISPECIFIC FUSION PROTEINS
; TITLE OF INVENTION: AND METHODS OF PRODUCING BIOLOGICALLY ACTIVE BISPECIFIC
; TITLE OF INVENTION: FUSION PROTEINS IN A MAMMALIAN CELL
; FILE REFERENCE: 30436.18USC1
; CURRENT APPLICATION NUMBER: US/09/549,067A
; CURRENT FILING DATE: 2000-04-13
; PRIOR APPLICATION NUMBER: 08/539,436
; PRIOR FILING DATE: 1995-10-05
; PRIOR APPLICATION NUMBER: 08/121,054
; PRIOR FILING DATE: 1993-09-13
; PRIOR APPLICATION NUMBER: 08/013,420
; PRIOR FILING DATE: 1993-02-01
; PRIOR APPLICATION NUMBER: 08/228,208
; PRIOR FILING DATE: 1994-04-15
; PRIOR APPLICATION NUMBER: 08/008,898
; PRIOR FILING DATE: 1993-01-22
; PRIOR APPLICATION NUMBER: 07/723,617
; PRIOR FILING DATE: 1991-06-27
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 18
; LENGTH: 302
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-549-067A-18
Query Match 72.3%; Score 952; DB 4; Length 302;
Best Local Similarity 75.8%; Pred. No. 4.1e-67;
Matches 191; Conservative 14; Mismatches 39; Indels 8; Gaps 3;
Qy 1 DIQMTOTSSLSASLGDRTVSCRASQDIRNLYNQKPDGTGVKFLIYVTSRLHPGVPS 60
Db 24 DIQMTOTSSLSASLGDRTVSCRASQDIRNLYNQKPDGTGVKFLIYVTSRLHPGVPS 83
Qy 61 RFSGSGSDTSLTINLQEDIGTYFCQGNTPMTFGGTTKLEIKRGGSDGGSGG 120
Db 84 RFSGSGSDTSLTIANLQPDIAFYCQGNTPMTFGGTTKLEIKRGGSDGGSGG 140
Qy 121 GSGGGGS--EVLQSGPELVKPGASVKISCKDSGYAFNSMNMVVKORPGQGLEWIGR 178
Db 141 GSGGGGSDIDEVQOQSGPELVKPGASMTWSCASGYSTGYIVNWLKQSHGNLEWIGL 200
Qy 179 IYPGDSNNGKFEKGKAILTADKSSSTAYMQLSSLTSDSVAVYFCARSGLL---RYAMD 235
Db 201 INPKGLTTYNQKFKGKATLTVDKSSSTAYMQLSSLTSDSVAVYFCARSGYGSDWYFD 260
Qy 236 YWGQTSVTVSS 247
Db 261 VWGAGTCTVSS 272

RESULT 5
US-09-813-659-30
; Sequence 30, Application US/09813659
; Patent No. 6482919
; GENERAL INFORMATION:
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Hayden, Martha S.
; APPLICANT: Linsley, Peter S.
; APPLICANT: Bajorath, Jurgen
; APPLICANT: Fell, H. Perry
; APPLICANT: Gilliland, Lisa K.
; TITLE OF INVENTION: EXPRESSION VECTORS ENCODING BISPECIFIC FUSION PROTEINS
; TITLE OF INVENTION: AND METHODS OF PRODUCING BIOLOGICALLY ACTIVE BISPECIFIC
; TITLE OF INVENTION: FUSION PROTEINS IN A MAMMALIAN CELL
; FILE REFERENCE: 30436.18USD2
; CURRENT APPLICATION NUMBER: US/09/813,659
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 09/549,067
; PRIOR FILING DATE: 2000-04-13
; PRIOR APPLICATION NUMBER: 08/539,436
; PRIOR FILING DATE: 1995-10-05
; PRIOR APPLICATION NUMBER: 08/121,054
; PRIOR FILING DATE: 1993-09-13
; PRIOR APPLICATION NUMBER: 08/013,420
; PRIOR FILING DATE: 1993-02-01
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 30
; LENGTH: 274
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-813-659-30
Query Match 72.3%; Score 951; DB 4; Length 274;
Best Local Similarity 75.8%; Pred. No. 4.4e-67;
Matches 191; Conservative 14; Mismatches 39; Indels 8; Gaps 3;
Qy 1 DIQMTOTSSLSASLGDRTVSCRASQDIRNLYNQKPDGTGVKFLIYVTSRLHPGVPS 60
Db 24 DIQMTOTSSLSASLGDRTVSCRASQDIRNLYNQKPDGTGVKFLIYVTSRLHPGVPS 83
Qy 61 RFSGSGSDTSLTINLQEDIGTYFCQGNTPMTFGGTTKLEIKRGGSDGGSGG 120
Db 84 RFSGSGSDTSLTIANLQPDIAFYCQGNTPMTFGGTTKLEIKRGGSDGGSGG 140
Qy 121 GSGGGGS--EVLQSGPELVKPGASVKISCKDSGYAFNSMNMVVKORPGQGLEWIGR 178
Db 141 GSGGGGSDIDEVQOQSGPELVKPGASMTWSCASGYSTGYIVNWLKQSHGNLEWIGL 200
Qy 179 IYPGDSNNGKFEKGKAILTADKSSSTAYMQLSSLTSDSVAVYFCARSGLL---RYAMD 235
Db 201 INPKGLTTYNQKFKGKATLTVDKSSSTAYMQLSSLTSDSVAVYFCARSGYGSDWYFD 260
Qy 236 YWGQTSVTVSS 247
Db 261 VWGAGTCTVSS 272

RESULT 6
US-09-549-067A-30
; Sequence 30, Application US/09549067A
; Patent No. 6623940
; GENERAL INFORMATION:
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Hayden, Martha S.
; APPLICANT: Linsley, Peter S.
; APPLICANT: Bajorath, Jurgen
; APPLICANT: Fell, H. Perry
; APPLICANT: Gilliland, Lisa K.
; TITLE OF INVENTION: EXPRESSION VECTORS ENCODING BISPECIFIC FUSION PROTEINS
; TITLE OF INVENTION: AND METHODS OF PRODUCING BIOLOGICALLY ACTIVE BISPECIFIC
; TITLE OF INVENTION: FUSION PROTEINS IN A MAMMALIAN CELL

FILE REFERENCE: 30436.18USC1
CURRENT APPLICATION NUMBER: US/09/549,067A
CURRENT FILING DATE: 2000-04-13
PRIOR APPLICATION NUMBER: 08/535,436
PRIOR FILING DATE: 1995-10-05
PRIOR APPLICATION NUMBER: 08/121,054
PRIOR FILING DATE: 1993-09-13
PRIOR APPLICATION NUMBER: 08/013,420
PRIOR FILING DATE: 1993-02-01
PRIOR APPLICATION NUMBER: 08/228,208
PRIOR FILING DATE: 1994-04-15
PRIOR APPLICATION NUMBER: 08/008,898
PRIOR FILING DATE: 1993-01-22
PRIOR APPLICATION NUMBER: 07/723,617
PRIOR FILING DATE: 1991-06-27
NUMBER OF SEQ ID NOS: 35
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 30
LENGTH: 274
TYPE: PRT
ORGANISM: Homo sapiens
US-09-549-067A-30

Query Match 72.3%; Score 951; DB 4; Length 274;
Best Local Similarity 75.8%; Pred. No. 4.4e-67;
Matches 191; Conservative 14; Mismatches 39; Indels 8; Gaps 3;

QY 1 DIQMTOTSSLSASLGRVTVSCRASQDIRNLYNNWYQKPDGTVKFLIYYTSRLLPGVPS 60
DB 24 DIQMTOTSSLSASLGRVTVSCRASQDIRNLYNNWYQKPDGTVKFLIYYTSRLHSGVPS 83

QY 61 RFGSGSGTDYSLTINNLEQEDIGTYFCQGNTPPWTFGGTKLEIKRGGSGDGGSGG 120
DB 84 RFGSGSGTDYSLTIANLPEDIAITYFCQGNTPPWTFGGTKLVTKRELG---GGSGG 140

QY 121 GSGSGGGS--EVQLQSGPELVKPGASVKISCKDGYAFNSSMMWVKQRPQGLEWIGR 178
DB 141 GSGSGGGSIDEVLQSGPELVKPGASMTMCSKASGYSTGYIVNWLKQSHGKNLEWIGL 200

QY 179 IYPGDGDSNYNGFEGKAILTADKSSSTAYMQLSSLTSDSVAYFCARSGLL---RYAMD 235
DB 201 INPKGLITTYNQKFKGKATLVTKSSSTAYMQLSSLTSDSVAYFCARSGYYGDSWDWYFD 260

QY 236 YWGQGTSTVTVSS 247
DB 261 VWGAGTTCVTVSS 272

RESULT 8
US-08-539-436-30
Sequence 30, Application US/08539436
Patent No. 6132992
GENERAL INFORMATION:
APPLICANT: Ledbetter, Jeffrey A.
APPLICANT: Gilliland, Lisa K.
APPLICANT: Hayden, Martha S.
APPLICANT: Linsley, Peter S.
APPLICANT: Bajorath, Jurgen
APPLICANT: Fell, Perry
TITLE OF INVENTION: Expression Vectors Encoding Bispecific
TITLE OF INVENTION: Fusion Proteins and Methods of Producing Biologically
TITLE OF INVENTION: Active Bispecific Fusion Proteins in a Mammalian Cell
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant & Gould
STREET: 11150 Santa Monica Blvd., Suite 400
CITY: Los Angeles
STATE: CA
COUNTRY: USA
ZIP: 90025
COMPUTER READABLE FORM: Floppy disk
MEDIUM TYPE: Floppy disk

FILE REFERENCE: 30436.18USC1
CURRENT APPLICATION NUMBER: US/09/549,067A
CURRENT FILING DATE: 2000-04-13
PRIOR APPLICATION NUMBER: 08/535,436
PRIOR FILING DATE: 1995-10-05
PRIOR APPLICATION NUMBER: 08/121,054
PRIOR FILING DATE: 1993-09-13
PRIOR APPLICATION NUMBER: 08/013,420
PRIOR FILING DATE: 1993-02-01
PRIOR APPLICATION NUMBER: 08/228,208
PRIOR FILING DATE: 1994-04-15
PRIOR APPLICATION NUMBER: 08/008,898
PRIOR FILING DATE: 1993-01-22
PRIOR APPLICATION NUMBER: 07/723,617
PRIOR FILING DATE: 1991-06-27
NUMBER OF SEQ ID NOS: 35
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 30
LENGTH: 274
TYPE: PRT
ORGANISM: Homo sapiens
US-09-549-067A-30

Query Match 72.3%; Score 951; DB 4; Length 274;
Best Local Similarity 75.8%; Pred. No. 4.4e-67;
Matches 191; Conservative 14; Mismatches 39; Indels 8; Gaps 3;

QY 1 DIQMTOTSSLSASLGRVTVSCRASQDIRNLYNNWYQKPDGTVKFLIYYTSRLLPGVPS 60
DB 24 DIQMTOTSSLSASLGRVTVSCRASQDIRNLYNNWYQKPDGTVKFLIYYTSRLHSGVPS 83

QY 61 RFGSGSGTDYSLTINNLEQEDIGTYFCQGNTPPWTFGGTKLEIKRGGSGDGGSGG 120
DB 84 RFGSGSGTDYSLTIANLPEDIAITYFCQGNTPPWTFGGTKLVTKRELG---GGSGG 140

QY 121 GSGSGGGS--EVQLQSGPELVKPGASVKISCKDGYAFNSSMMWVKQRPQGLEWIGR 178
DB 141 GSGSGGGSIDEVLQSGPELVKPGASMTMCSKASGYSTGYIVNWLKQSHGKNLEWIGL 200

QY 179 IYPGDGDSNYNGFEGKAILTADKSSSTAYMQLSSLTSDSVAYFCARSGLL---RYAMD 235
DB 201 INPKGLITTYNQKFKGKATLVTKSSSTAYMQLSSLTSDSVAYFCARSGYYGDSWDWYFD 260

QY 236 YWGQGTSTVTVSS 247
DB 261 VWGAGTTCVTVSS 272

RESULT 7
US-08-121-054C-30
Sequence 30, Application US/08121054C
Patent No. 5637481
GENERAL INFORMATION:
APPLICANT: Ledbetter, Jeffrey A.
APPLICANT: Gilliland, Lisa K.
APPLICANT: Hayden, Martha S.
APPLICANT: Linsley, Peter S.
APPLICANT: Bajorath, Jurgen
APPLICANT: Fell, Perry
TITLE OF INVENTION: Expression Vectors Encoding Bispecific
TITLE OF INVENTION: Fusion Proteins and Methods of Producing Biologically
TITLE OF INVENTION: Active Bispecific Fusion Proteins in a Mammalian Cell
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant & Gould
STREET: 11150 Santa Monica Blvd., Suite 400
CITY: Los Angeles
STATE: CA
COUNTRY: USA
ZIP: 90025
COMPUTER READABLE FORM: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/539,436
FILING DATE: 05-OCT-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/121,054
FILING DATE: 13-SEP-1993
APPLICATION NUMBER: US 08/013,420
FILING DATE: 01-FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME: Adriano, Sarah B.
REGISTRATION NUMBER: 34,470
REFERENCE/DOCKET NUMBER: 30436.18US01
TELEPHONE: 310-445-1140
TELEFAX: 310-445-9031
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 302 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-539-436-30

Query Match 72.3%; Score 951; DB 3; Length 302;
Best Local Similarity 75.8%; Pred. No. 4.9e-67;
Matches 191; Conservative 14; Mismatches 39; Indels 8; Gaps 3;

1 DIQMTQTSSLSASLGRVTVSCRASQDIRNLNWKQKPDGTGKFLIYVTSRLPGVPS 60
24 DIQMTQTSSLSASLGRVTVSCRASQDIRNLNWKQKPDGTGKFLIYVTSRLHSGVPS 83
61 RFGSGSGTDYSLTNNLEQEDIGTYFCQCGNTPPWTFGGGTGKLEIKRGGSGDGGSGG 120
84 RFGSGSGTDYSLTNNLEQEDIGTYFCQCGNTPPWTFGGGTGKLEIKRGGSGDGGSGG 140
121 GSGSGGGS--EVQLQSQGPPELVKPGASVKISCKDSTGAFNNSWMNVKQRPQGLEWIGR 178
141 GSGSGGGSIDEVQLQSQGPPELVKPGASVTMSCKASGYSFTGYIYNWLKQSHGNLEWIGL 200
179 IYPGDSNNGKPFEGKAILTADKSSSTAYWQLSLSVDSAVYFCARSGLL---RYAMD 235
201 INPYKGLTNYNQKFGKATLTVDKSSSTAYWQLSLSVDSAVYFCARSGYDSDWYFD 260
236 YMGQGTSTVSS 247
261 VVGAGTCTVSS 272

US-09-813-659-32

Query Match 72.3%; Score 951; DB 4; Length 302;
Best Local Similarity 75.8%; Pred. No. 4.9e-67;
Matches 191; Conservative 14; Mismatches 39; Indels 8; Gaps 3;

1 DIQMTQTSSLSASLGRVTVSCRASQDIRNLNWKQKPDGTGKFLIYVTSRLPGVPS 60
24 DIQMTQTSSLSASLGRVTVSCRASQDIRNLNWKQKPDGTGKFLIYVTSRLHSGVPS 83
61 RFGSGSGTDYSLTNNLEQEDIGTYFCQCGNTPPWTFGGGTGKLEIKRGGSGDGGSGG 120
84 RFGSGSGTDYSLTNNLEQEDIGTYFCQCGNTPPWTFGGGTGKLEIKRGGSGDGGSGG 140
121 GSGSGGGS--EVQLQSQGPPELVKPGASVKISCKDSTGAFNNSWMNVKQRPQGLEWIGR 178
141 GSGSGGGSIDEVQLQSQGPPELVKPGASVTMSCKASGYSFTGYIYNWLKQSHGNLEWIGL 200
179 IYPGDSNNGKPFEGKAILTADKSSSTAYWQLSLSVDSAVYFCARSGLL---RYAMD 235
201 INPYKGLTNYNQKFGKATLTVDKSSSTAYWQLSLSVDSAVYFCARSGYDSDWYFD 260
236 YMGQGTSTVSS 247
261 VVGAGTCTVSS 272

US-09-549-067A-32

Query Match 72.3%; Score 951; DB 4; Length 302;
Best Local Similarity 75.8%; Pred. No. 4.9e-67;
Matches 191; Conservative 14; Mismatches 39; Indels 8; Gaps 3;

1 DIQMTQTSSLSASLGRVTVSCRASQDIRNLNWKQKPDGTGKFLIYVTSRLPGVPS 60
24 DIQMTQTSSLSASLGRVTVSCRASQDIRNLNWKQKPDGTGKFLIYVTSRLHSGVPS 83
61 RFGSGSGTDYSLTNNLEQEDIGTYFCQCGNTPPWTFGGGTGKLEIKRGGSGDGGSGG 120
84 RFGSGSGTDYSLTNNLEQEDIGTYFCQCGNTPPWTFGGGTGKLEIKRGGSGDGGSGG 140
121 GSGSGGGS--EVQLQSQGPPELVKPGASVKISCKDSTGAFNNSWMNVKQRPQGLEWIGR 178
141 GSGSGGGSIDEVQLQSQGPPELVKPGASVTMSCKASGYSFTGYIYNWLKQSHGNLEWIGL 200
179 IYPGDSNNGKPFEGKAILTADKSSSTAYWQLSLSVDSAVYFCARSGLL---RYAMD 235
201 INPYKGLTNYNQKFGKATLTVDKSSSTAYWQLSLSVDSAVYFCARSGYDSDWYFD 260
236 YMGQGTSTVSS 247
261 VVGAGTCTVSS 272

US-09-549-067A-32

Query Match 72.3%; Score 951; DB 4; Length 302;
Best Local Similarity 75.8%; Pred. No. 4.9e-67;
Matches 191; Conservative 14; Mismatches 39; Indels 8; Gaps 3;

1 DIQMTQTSSLSASLGRVTVSCRASQDIRNLNWKQKPDGTGKFLIYVTSRLPGVPS 60
24 DIQMTQTSSLSASLGRVTVSCRASQDIRNLNWKQKPDGTGKFLIYVTSRLHSGVPS 83
61 RFGSGSGTDYSLTNNLEQEDIGTYFCQCGNTPPWTFGGGTGKLEIKRGGSGDGGSGG 120
84 RFGSGSGTDYSLTNNLEQEDIGTYFCQCGNTPPWTFGGGTGKLEIKRGGSGDGGSGG 140
121 GSGSGGGS--EVQLQSQGPPELVKPGASVKISCKDSTGAFNNSWMNVKQRPQGLEWIGR 178
141 GSGSGGGSIDEVQLQSQGPPELVKPGASVTMSCKASGYSFTGYIYNWLKQSHGNLEWIGL 200
179 IYPGDSNNGKPFEGKAILTADKSSSTAYWQLSLSVDSAVYFCARSGLL---RYAMD 235
201 INPYKGLTNYNQKFGKATLTVDKSSSTAYWQLSLSVDSAVYFCARSGYDSDWYFD 260
236 YMGQGTSTVSS 247
261 VVGAGTCTVSS 272

US-09-549-067A-32

Query Match 72.3%; Score 951; DB 4; Length 302;
Best Local Similarity 75.8%; Pred. No. 4.9e-67;
Matches 191; Conservative 14; Mismatches 39; Indels 8; Gaps 3;

1 DIQMTQTSSLSASLGRVTVSCRASQDIRNLNWKQKPDGTGKFLIYVTSRLPGVPS 60
24 DIQMTQTSSLSASLGRVTVSCRASQDIRNLNWKQKPDGTGKFLIYVTSRLHSGVPS 83
61 RFGSGSGTDYSLTNNLEQEDIGTYFCQCGNTPPWTFGGGTGKLEIKRGGSGDGGSGG 120
84 RFGSGSGTDYSLTNNLEQEDIGTYFCQCGNTPPWTFGGGTGKLEIKRGGSGDGGSGG 140
121 GSGSGGGS--EVQLQSQGPPELVKPGASVKISCKDSTGAFNNSWMNVKQRPQGLEWIGR 178
141 GSGSGGGSIDEVQLQSQGPPELVKPGASVTMSCKASGYSFTGYIYNWLKQSHGNLEWIGL 200
179 IYPGDSNNGKPFEGKAILTADKSSSTAYWQLSLSVDSAVYFCARSGLL---RYAMD 235
201 INPYKGLTNYNQKFGKATLTVDKSSSTAYWQLSLSVDSAVYFCARSGYDSDWYFD 260
236 YMGQGTSTVSS 247
261 VVGAGTCTVSS 272

US-09-549-067A-32

Query Match 72.3%; Score 951; DB 4; Length 302;
Best Local Similarity 75.8%; Pred. No. 4.9e-67;
Matches 191; Conservative 14; Mismatches 39; Indels 8; Gaps 3;

1 DIQMTQTSSLSASLGRVTVSCRASQDIRNLNWKQKPDGTGKFLIYVTSRLPGVPS 60
24 DIQMTQTSSLSASLGRVTVSCRASQDIRNLNWKQKPDGTGKFLIYVTSRLHSGVPS 83
61 RFGSGSGTDYSLTNNLEQEDIGTYFCQCGNTPPWTFGGGTGKLEIKRGGSGDGGSGG 120
84 RFGSGSGTDYSLTNNLEQEDIGTYFCQCGNTPPWTFGGGTGKLEIKRGGSGDGGSGG 140
121 GSGSGGGS--EVQLQSQGPPELVKPGASVKISCKDSTGAFNNSWMNVKQRPQGLEWIGR 178
141 GSGSGGGSIDEVQLQSQGPPELVKPGASVTMSCKASGYSFTGYIYNWLKQSHGNLEWIGL 200
179 IYPGDSNNGKPFEGKAILTADKSSSTAYWQLSLSVDSAVYFCARSGLL---RYAMD 235
201 INPYKGLTNYNQKFGKATLTVDKSSSTAYWQLSLSVDSAVYFCARSGYDSDWYFD 260
236 YMGQGTSTVSS 247
261 VVGAGTCTVSS 272

US-09-549-067A-32

Query Match 72.3%; Score 951; DB 4; Length 302;
Best Local Similarity 75.8%; Pred. No. 4.9e-67;
Matches 191; Conservative 14; Mismatches 39; Indels 8; Gaps 3;

1 DIQMTQTSSLSASLGRVTVSCRASQDIRNLNWKQKPDGTGKFLIYVTSRLPGVPS 60
24 DIQMTQTSSLSASLGRVTVSCRASQDIRNLNWKQKPDGTGKFLIYVTSRLHSGVPS 83
61 RFGSGSGTDYSLTNNLEQEDIGTYFCQCGNTPPWTFGGGTGKLEIKRGGSGDGGSGG 120
84 RFGSGSGTDYSLTNNLEQEDIGTYFCQCGNTPPWTFGGGTGKLEIKRGGSGDGGSGG 140
121 GSGSGGGS--EVQLQSQGPPELVKPGASVKISCKDSTGAFNNSWMNVKQRPQGLEWIGR 178
141 GSGSGGGSIDEVQLQSQGPPELVKPGASVTMSCKASGYSFTGYIYNWLKQSHGNLEWIGL 200
179 IYPGDSNNGKPFEGKAILTADKSSSTAYWQLSLSVDSAVYFCARSGLL---RYAMD 235
201 INPYKGLTNYNQKFGKATLTVDKSSSTAYWQLSLSVDSAVYFCARSGYDSDWYFD 260
236 YMGQGTSTVSS 247
261 VVGAGTCTVSS 272

US-09-549-067A-32

Query Match 72.3%; Score 951; DB 4; Length 302;
Best Local Similarity 75.8%; Pred. No. 4.9e-67;
Matches 191; Conservative 14; Mismatches 39; Indels 8; Gaps 3;

1 DIQMTQTSSLSASLGRVTVSCRASQDIRNLNWKQKPDGTGKFLIYVTSRLPGVPS 60
24 DIQMTQTSSLSASLGRVTVSCRASQDIRNLNWKQKPDGTGKFLIYVTSRLHSGVPS 83
61 RFGSGSGTDYSLTNNLEQEDIGTYFCQCGNTPPWTFGGGTGKLEIKRGGSGDGGSGG 120
84 RFGSGSGTDYSLTNNLEQEDIGTYFCQCGNTPPWTFGGGTGKLEIKRGGSGDGGSGG 140
121 GSGSGGGS--EVQLQSQGPPELVKPGASVKISCKDSTGAFNNSWMNVKQRPQGLEWIGR 178
141 GSGSGGGSIDEVQLQSQGPPELVKPGASVTMSCKASGYSFTGYIYNWLKQSHGNLEWIGL 200
179 IYPGDSNNGKPFEGKAILTADKSSSTAYWQLSLSVDSAVYFCARSGLL---RYAMD 235
201 INPYKGLTNYNQKFGKATLTVDKSSSTAYWQLSLSVDSAVYFCARSGYDSDWYFD 260
236 YMGQGTSTVSS 247
261 VVGAGTCTVSS 272

US-09-549-067A-32

Query Match 72.3%; Score 951; DB 4; Length 302;
Best Local Similarity 75.8%; Pred. No. 4.9e-67;
Matches 191; Conservative 14; Mismatches 39; Indels 8; Gaps 3;

1 DIQMTQTSSLSASLGRVTVSCRASQDIRNLNWKQKPDGTGKFLIYVTSRLPGVPS 60
24 DIQMTQTSSLSASLGRVTVSCRASQDIRNLNWKQKPDGTGKFLIYVTSRLHSGVPS 83
61 RFGSGSGTDYSLTNNLEQEDIGTYFCQCGNTPPWTFGGGTGKLEIKRGGSGDGGSGG 120
84 RFGSGSGTDYSLTNNLEQEDIGTYFCQCGNTPPWTFGGGTGKLEIKRGGSGDGGSGG 140
121 GSGSGGGS--EVQLQSQGPPELVKPGASVKISCKDSTGAFNNSWMNVKQRPQGLEWIGR 178
141 GSGSGGGSIDEVQLQSQGPPELVKPGASVTMSCKASGYSFTGYIYNWLKQSHGNLEWIGL 200
179 IYPGDSNNGKPFEGKAILTADKSSSTAYWQLSLSVDSAVYFCARSGLL---RYAMD 235
201 INPYKGLTNYNQKFGKATLTVDKSSSTAYWQLSLSVDSAVYFCARSGYDSDWYFD 260
236 YMGQGTSTVSS 247
261 VVGAGTCTVSS 272

US-09-549-067A-32

Query Match 72.3%; Score 951; DB 4; Length 302;
Best Local Similarity 75.8%; Pred. No. 4.9e-67;
Matches 191; Conservative 14; Mismatches 39; Indels 8; Gaps 3;

1 DIQMTQTSSLSASLGRVTVSCRASQDIRNLNWKQKPDGTGKFLIYVTSRLPGVPS 60
24 DIQMTQTSSLSASLGRVTVSCRASQDIRNLNWKQKPDGTGKFLIYVTSRLHSGVPS 83
61 RFGSGSGTDYSLTNNLEQEDIGTYFCQCGNTPPWTFGGGTGKLEIKRGGSGDGGSGG 120
84 RFGSGSGTDYSLTNNLEQEDIGTYFCQCGNTPPWTFGGGTGKLEIKRGGSGDGGSGG 140
121 GSGSGGGS--EVQLQSQGPPELVKPGASVKISCKDSTGAFNNSWMNVKQRPQGLEWIGR 178
141 GSGSGGGSIDEVQLQSQGPPELVKPGASVTMSCKASGYSFTGYIYNWLKQSHGNLEWIGL 200
179 IYPGDSNNGKPFEGKAILTADKSSSTAYWQLSLSVDSAVYFCARSGLL---RYAMD 235
201 INPYKGLTNYNQKFGKATLTVDKSSSTAYWQLSLSVDSAVYFCARSGYDSDWYFD 260
236 YMGQGTSTVSS 247
261 VVGAGTCTVSS 272

US-09-549-067A-32

Query Match 72.3%; Score 951; DB 4; Length 302;
Best Local Similarity 75.8%; Pred. No. 4.9e-67;
Matches 191; Conservative 14; Mismatches 39; Indels 8; Gaps 3;

Query Match 72.3%; Score 951; DB 4; Length 302;
Best Local Similarity 75.8%; Pred. No. 4.9e-67;
Matches 191; Conservative 14; Mismatches 39; Indels 8; Gaps 3;

QY 1 DIQMTQTSSLSASLGRVTVSCRASQDIRNYLNWYQKPDGTGKFLIYTSRLPGVPS 60
DB 24 DIQMTQTSSLSASLGRVTVSCRASQDIRNYLNWYQKPDGTGKFLIYTSRLPGVPS 83

QY 61 RPSGSGGTDSLNNLEQEDIGTYFCQCGNTPTWTFGGTGLKLEIKRGGSGDGGSGG 120
DB 84 RPSGSGGTDSLNNLEQEDIGTYFCQCGNTPTWTFGGTGLKLEIKRGGSGDGGSGG 140

QY 121 GSGGGGGS--EVQLQQSGPELVKPGASVKISCKDSGYAFNNSMNNWYKQPGGLEWIGR 178
DB 141 GSGGGGGSIDEVQLQQSGPELVKPGASMTMCKASGYFTGIYVNLKQSHKQNLWIGL 200

QY 179 IYPGDDSNYNGKFEKGAITLADKSSSTAYMQLSSLTSDSAVYFCARSGLL---RYAMD 235
DB 201 INPYKGLTYNQKFKGKATLTVDKSSSTAYMQLSSLTSDSAVYFCARSGLL---RYAMD 260

QY 236 YVQGGTSTVSS 247
DB 261 VWGAGTTCTVSS 272

RESULT 11
US-08-400-115-4
; Sequence 4, Application US/08400115
; Patent No. 5864019
; GENERAL INFORMATION:
; APPLICANT: KING, David John
; APPLICANT: MOUNTAIN, Andrew
; APPLICANT: OWENS, Raymond John
; APPLICANT: YARRANTON, Geoffrey Thomas
; TITLE OF INVENTION: Multivalent Antigen-Binding Proteins
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; APPLICATION NUMBER: US/08/400,115
; FILING DATE: 06-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/127,136
; FILING DATE: 27-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/842,193
; FILING DATE: 17-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB91/00935
; FILING DATE: 11-JUN-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9012995.8
; FILING DATE: 11-JUN-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: ISACSON, John P.
; REGISTRATION NUMBER: 33,715
; REFERENCE/DOCKET NUMBER: 040283/0106 CARA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:

LENGTH: 271 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-400-115-4

Query Match 62.2%; Score 819; DB 2; Length 271;
Best Local Similarity 65.6%; Pred. No. 9e-57;
Matches 162; Conservative 28; Mismatches 47; Indels 10; Gaps 2;

QY 1 DIQMTQTSSLSASLGRVTVSCRASQDIRNYLNWYQKPDGTGKFLIYTSRLPGVPS 60
DB 23 DIQMTQSPASLSVSGETVITCRASENIYSLNAMYQKQKSPQLLYAATNLADGVPS 82

QY 61 RPSGSGGTDSLNNLEQEDIGTYFCQCGNTPTWTFGGTGLKLEIKRGGSGDGGSGG 120
DB 83 RPSGSGGTDSLNNLEQEDIGTYFCQCGNTPTWTFGGTGLKLEIKRGGSGDGGSGG 137

QY 121 GSGGGGGSVQLQQSGPELVKPGASVKISCKDSGYAFNNSMNNWYKQPGGLEWIGRIY 180
DB 138 GSGGGGGSVQLQQSGPELVKPGASVKISCKDSGYAFNNSMNNWYKQPGGLEWIGRIY 197

QY 181 PGDGSNNGKFEKGAITLADKSSSTAYMQLSSLTSDSAVYFCARSGLLRYAMDYWGQ 240
DB 198 PGNDIKYNEKFKGKATLTVDKSSSTAYMQLSSLTSDSAVYFCARSGLLRYAMDYWGQ 252

QY 241 TSVTVSS 247
DB 253 TILTVSS 259

RESULT 12
US-08-875-811-41
; Sequence 41, Application US/08875811
; Patent No. 6045793
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: Boque, Lluís
; APPLICANT: Wlodawer, Alexander
; TITLE OF INVENTION: Recombinant Ribonuclease Proteins
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/875,811
; FILING DATE: 19-FEB-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/02588
; FILING DATE: 19-FEB-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/011,800
; FILING DATE: 21-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Faris, Susan K.
; REGISTRATION NUMBER: 41,739
; REFERENCE/DOCKET NUMBER: 015280-244100US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 41:
; SEQUENCE CHARACTERISTICS:

LENGTH: 355 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-875-811-49

Query Match 61.7%; Score 812; DB 3; Length 355;
 Best Local Similarity 64.8%; Pred. No. 4.2e-56;
 Matches 160; Conservative 33; Mismatches 44; Indels 10; Gaps 2;

QY	1	DIOMTQTSSLSASIGDRVTVSCRASQDIRNLYNWYQOKPDGTGVKFLIYTSRLPGVPS	60
DB	1	DIKMTQSPSSMYASIGERVTFCKASQDINNLCWFQKPKGSKPTLIYRANRLVDGVP	60
QY	61	RFSGSGSDYSLTINNLEQEDIGTYFCQGNTPPWTFGGTKLEIKRGGSGDGGSGG	120
DB	61	RFSGSGSDYSLTINNLEQEDIGTYFCQGNTPPWTFGGTKLEIKRGGSGDGGSGG	114
QY	121	GGSGGGSEVQLQSGGVLPKPGASVKISCKDSGVAFNSMWNVVKORPGQGLEWIGRIY	180
DB	115	GGSGGGSEVQLQSGGVLPKPGASVKISCKDSGVAFNSMWNVVKORPGQGLEWIGRIY	174
QY	181	PDGDSNYNKGPEKAILTADKSSSTAYMQLSSLTSDVSADVFCARGLRLYANDYWGQ	240
DB	175	PRNSDTIYNPQFKHAKLTAVTSTAYMELNSLTNEDSAVYYCTP----	230
QY	241	TSVTSS 247	
DB	231	TLTVSS 237	

RESULT 14
 US-08-875-811-64
 Sequence 64, Application US/08875811
 Patent No. 6045793
 GENERAL INFORMATION:
 APPLICANT: Rybak, Susanna M.
 APPLICANT: Newton, Dianne L.
 APPLICANT: Boque, Luis
 APPLICANT: Wlodawer, Alexander
 TITLE OF INVENTION: Recombinant Ribonuclease Proteins
 NUMBER OF SEQUENCES: 64
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend and Crew LLP
 STREET: Two Embarcadero Center, Eighth Floor
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94111-3834
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/875,811
 FILING DATE: 19-FEB-1998
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: WO PCT/US97/02588
 FILING DATE: 19-FEB-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/011,800
 FILING DATE: 21-FEB-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Paris, Susan K.
 REGISTRATION NUMBER: 41,739
 REFERENCE/DOCKET NUMBER: 015280-244100US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 576-0200
 TELEFAX: (415) 576-0300
 INFORMATION FOR SEQ ID NO: 64:
 SEQUENCE CHARACTERISTICS:

LENGTH: 355 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-875-811-41

Query Match 61.7%; Score 812; DB 3; Length 355;
 Best Local Similarity 64.8%; Pred. No. 4.2e-56;
 Matches 160; Conservative 33; Mismatches 44; Indels 10; Gaps 2;

QY	1	DIOMTQTSSLSASIGDRVTVSCRASQDIRNLYNWYQOKPDGTGVKFLIYTSRLPGVPS	60
DB	1	DIKMTQSPSSMYASIGERVTFCKASQDINNLCWFQKPKGSKPTLIYRANRLVDGVP	60
QY	61	RFSGSGSDYSLTINNLEQEDIGTYFCQGNTPPWTFGGTKLEIKRGGSGDGGSGG	120
DB	61	RFSGSGSDYSLTINNLEQEDIGTYFCQGNTPPWTFGGTKLEIKRGGSGDGGSGG	114
QY	121	GGSGGGSEVQLQSGGVLPKPGASVKISCKDSGVAFNSMWNVVKORPGQGLEWIGRIY	180
DB	115	GGSGGGSEVQLQSGGVLPKPGASVKISCKDSGVAFNSMWNVVKORPGQGLEWIGRIY	174
QY	181	PDGDSNYNKGPEKAILTADKSSSTAYMQLSSLTSDVSADVFCARGLRLYANDYWGQ	240
DB	175	PRNSDTIYNPQFKHAKLTAVTSTAYMELNSLTNEDSAVYYCTP----	230
QY	241	TSVTSS 247	
DB	231	TLTVSS 237	

RESULT 13
 US-08-875-811-49
 Sequence 49, Application US/08875811
 Patent No. 6045793
 GENERAL INFORMATION:
 APPLICANT: Rybak, Susanna M.
 APPLICANT: Newton, Dianne L.
 APPLICANT: Boque, Luis
 APPLICANT: Wlodawer, Alexander
 TITLE OF INVENTION: Recombinant Ribonuclease Proteins
 NUMBER OF SEQUENCES: 64
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend and Crew LLP
 STREET: Two Embarcadero Center, Eighth Floor
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94111-3834
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/875,811
 FILING DATE: 19-FEB-1998
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: WO PCT/US97/02588
 FILING DATE: 19-FEB-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/011,800
 FILING DATE: 21-FEB-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Paris, Susan K.
 REGISTRATION NUMBER: 41,739
 REFERENCE/DOCKET NUMBER: 015280-244100US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 576-0200
 TELEFAX: (415) 576-0300
 INFORMATION FOR SEQ ID NO: 49:
 SEQUENCE CHARACTERISTICS:

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; LENGTH: 355 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..355
; OTHER INFORMATION: /note="B6FB[Met-(-1)]SerrOnc"
US-08-875-811-64

Query Match 61.7%; Score 812; DB 3; Length 355;
Best Local Similarity 64.8%; Pred.No. 4.2e-56;
Matches 160; Conservative 33; Mismatches 44; Indels 10; Gaps 2;

QY 1 DIQMTQTTSSLSASLGRVTVSCRASQDIRNLYNQKPDGTVKFLIYYTSRLLPGVPS 60
Db 1 DIKMTQSPSSMYASLGERVTFCKASQDINNYLQFQKPGKSPKTLIYRANRLVDGVPS 60
QY 61 RFGSGSGTDYSLTINNLEQEDIGTYFCQGNTPMTFGGKLEIKRGGSGDGGSGG 120
Db 61 RFGSGSGQDYSLTSSLEVEDMGIYYCQYDEFFPYFGGKLEIK-----GGGSGG 114
QY 121 GSGSGGSEVQLQSQSGTVLARPASVYKMSCKASGYTFSSYWHWIKORPGQGLDWI 180
Db 115 GSGSGGSEVQLQSQSGTVLARPASVYKMSCKASGYTFSSYWHWIKORPGQGLDWI 174
QY 181 PGDSDNYNGKEGKAILLTADKSSSTAYMQLSLSVDSAVYFCARSGLLRYANDYWG 240
Db 175 PRNSDTIYNQFQKHAKLTAVTSTSTAYMELNSLTNEDSAVYYCTP-----LYYFDSWG 230
QY 241 TSVTVSS 247
Db 231 TLTVSS 237

TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 358 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-875-811-45

Query Match 61.7%; Score 812; DB 3; Length 358;
Best Local Similarity 64.8%; Pred.No. 4.3e-56;
Matches 160; Conservative 33; Mismatches 44; Indels 10; Gaps 2;

QY 1 DIQMTQTTSSLSASLGRVTVSCRASQDIRNLYNQKPDGTVKFLIYYTSRLLPGVPS 60
Db 119 DIRMTQSPSSMYASLGERVTFCKASQDINNYLQFQKPGKSPKTLIYRANRLVDGVPS 178
QY 61 RFGSGSGTDYSLTINNLEQEDIGTYFCQGNTPMTFGGKLEIKRGGSGDGGSGG 120
Db 179 RFGSGSGQDYSLTSSLEVEDMGIYYCQYDEFFPYFGGKLEIK-----GGGSGG 232
QY 121 GSGSGGSEVQLQSQSGTVLARPASVYKMSCKASGYTFSSYWHWIKORPGQGLDWI 180
Db 233 GSGSGGSEVQLQSQSGTVLARPASVYKMSCKASGYTFSSYWHWIKORPGQGLDWI 292
QY 181 PGDSDNYNGKEGKAILLTADKSSSTAYMQLSLSVDSAVYFCARSGLLRYANDYWG 240
Db 293 PRNSDTIYNQFQKHAKLTAVTSTSTAYMELNSLTNEDSAVYYCTP-----LYYFDSWG 348
QY 241 TSVTVSS 247
Db 349 TLTVSS 355
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Job time : 17.5 secs

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RESULT 15
US-08-875-811-45
; Sequence 45, Application US/08875811
; Patent No. 6045793
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: Boque, Lluis
; APPLICANT: Wlodawer, Alexander
; TITLE OF INVENTION: Recombinant Ribonuclease Proteins
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/875,811
; FILING DATE: 19-FEB-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/02588
; FILING DATE: 19-FEB-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/011,800
; FILING DATE: 21-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Faris, Susan K.
; REGISTRATION NUMBER: 41,739
; REFERENCE/DOCKET NUMBER: 015280-24410005
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OM protein - protein search, using sw model

Run on: April 22, 2004, 11:45:27 ; Search time 51 Seconds
(without alignments)
1368.416 Million cell updates/sec

Title: US-10-620-049-25
Perfect score: 1316
Sequence: 1 DIQWQTSSLSASLGRVT.....GLLRVANDVWGQTSVTSS 247

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : A_Geneseq_23Jan04.*
- 1: Geneseq1980s.*
 - 2: Geneseq1990s.*
 - 3: Geneseq2000s.*
 - 4: Geneseq2001s.*
 - 5: Geneseq2002s.*
 - 6: Geneseq2003as.*
 - 7: Geneseq2003bs.*
 - 8: Geneseq2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1246	94.7	247	AAO27254	Antibody
2	1243	94.5	247	AAO27253	Antibody
3	1242	94.4	247	AAO27255	Antibody
4	1235	93.8	247	AAO27252	Antibody
5	1230	93.5	247	AAO27256	Antibody
6	991	75.3	637	AAU75365	Diphtheri
7	991	75.3	638	AAU75370	Diphtheri
8	991	75.3	656	AAU75383	Immunotox
9	991	75.3	657	AAU75389	Diphtheri
10	989	75.2	601	ABG07461	An immuno
11	989	75.2	601	ABG72265	Recombina
12	989	75.2	642	AAU75382	Diphtheri
13	989	75.2	642	AAO29675	Anti-T ce
14	989	75.2	643	AAU75390	Diphtheri
15	989	75.2	643	AAO29670	Anti-T ce
16	985.5	74.9	895	AAU75369	Diphtheri
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19	985.5	74.9	895	AAO29673	Anti-T ce
20	985.5	74.9	896	AAU75367	Diphtheri
21	985.5	74.9	896	AAU75366	Diphtheri
22	985.5	74.9	896	AAU75373	Diphtheri
23	985.5	74.9	896	AAO29672	Anti-T ce
24	985.5	74.9	896	AAO29671	Anti-T ce
25	985.5	74.9	896	AAO29676	Anti-T ce

26	985.5	74.9	899	5	AAU75375	AAU75375 Diphtheri
27	985.5	74.9	899	6	AAO29674	Anti-T ce
28	981.5	74.6	652	5	AAU75448	Immunotox
29	956.5	72.7	554	3	AAU50822	Fv-antibo
30	951	72.3	302	2	AAU60206	Bispecifi
31	945	71.8	504	7	ADD25787	Binding d
32	945	71.8	555	7	AD86039	Anti-CD3
33	924	70.2	562	6	ABE57058	Plasmid p
34	923.5	70.2	531	3	AAU43749	Amino aci
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36	914	69.5	271	7	ADD25451	Binding d
37	890	67.6	251	4	AAU74793	Single ch
38	890	67.6	258	4	AAU74794	Single ch
39	883	67.1	543	7	ADD12876	CD28/mela
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41	871	66.2	539	3	AAU50823	Fv-antibo
42	869	66.0	562	6	ABE57059	Plasmid p
43	848.5	64.5	436	3	AAU91026	Apoptobod
44	845	64.2	650	6	ABR62591	Anti-CD7
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ALIGNMENTS

RESULT 1
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ID AAO27254 standard; protein; 247 AA.
XX
AC AAO27254;
XX
DT 17-SEP-2003 (first entry)
XX
DE Antibody 14B7 scFv mutant 1H amino acid sequence.
XX
KW Mouse; murine; affinity-matured recombinant antibody;
KW proteinaceous toxin; Bacillus anthracis protective antigen;
KW antibacterial; gene therapy; vaccine; biological warfare agent;
KW infection; hybridoma; scFv; 14B7; mutant; mutein; 1H.
XX
OS Mus sp.
OS Synthetic.
XX
FH Key
FT Region 1. .108 Location/Qualifiers
FT Region 1. .23 /label= Light_chain
FT Region /label= LFR1
FT Region /note= "Light chain framework region 1"
FT Region 24. .34 /label= CDR_L1
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FT Region 35. .49 /label= LFR2
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FT Region 50. .56 /label= CDR_L2
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FT Misc-difference 55 /note= "Wild-type Gln substituted by Leu"
FT Misc-difference 56 /note= "Wild-type Ser substituted by Pro"
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FT Region /label= "Light chain framework region 3"
FT Region 89. .97 /label= CDR_L3
FT Region /label= "Complementarity determining region L3"
FT Region 98. .108 /label= LFR4
FT Region /label= "Light chain framework region 4"
FT Misc-difference 107 /note= "Wild-type Lys substituted by Arg"
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FT	Region	109..128 /label= linker /note= "(Gly4Ser)4 linker"
FT	Region	129..247 /label= Heavy_chain
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FT	Region	155..163 /label= CDR_H1 /note= "Complementarity determining region H1"
FT	Region	164..177 /label= HFR2 /note= "Heavy chain framework region 2"
FT	Region	178..194 /label= CDR_H2 /note= "Complementarity determining region H2"
FT	Region	195..226 /label= HFR3 /note= "Heavy chain framework region 3"
FT	Region	227..236 /label= CDR_H3 /note= "Complementarity determining region H3"
FT	Region	237..247 /label= HFR4 /note= "Heavy chain framework region 4"
XX	WO2003040384-A1.	
PX	15-MAY-2003.	
XX	05-NOV-2002; 2002WO-US035567.	
XX	05-NOV-2001; 2001US-0332849P.	
XX	(TEXA) UNIV TEXAS SYSTEM.	
XX	Georgiou G, Iverson BL, Maynard JA;	
XX	WPI; 2003-430672/40.	
XX	New purified affinity-matured recombinant antibody with binding specificity for Bacillus anthracis protective antigen, useful for diagnosing, preventing or treating anthrax or other bacterial infections.	
PS	Example; Page; 48pp; English.	
CC	This invention relates a purified affinity-matured recombinant antibody or its portion having binding specificity for a proteinaceous toxin or a Bacillus anthracis protective antigen. The antibody may have an antibacterial activity and may be used in gene therapy or a vaccine.	
CC	Bacillus anthracis, commonly referred to as was one of the first biological warfare agents to be developed and is now perceived as a major threat worldwide. The composition and methods of the invention may be useful in diagnosing, preventing or treating infections caused by Bacillus anthracis and other bacterial toxins. The present sequence is that of the mouse wild-type anti-protective antigen hybridoma antibody 14B7 scFv mutant 1H, with a synthetic linker (Gly4Ser) ⁴ between the light and heavy chains. This antibody had Gln55Leu, Ser56Pro and Lys107Arg substitutions compared to the wild-type sequence (see AAO27252) and was developed in the examples of the specification in order to identify antibodies which had increased binding affinity for the Bacillus anthracis toxin. Note: This sequence does not appear in the specification but was created by the indexer using information given in the examples and figure 4 of the disclosure	
SQ	Sequence 247 AA;	
Query Match	94.7%; Score 1246; DB 6; Length 247;	
Best Local Similarity	94.7%; Pred.No.3.e-77;	
Matches 234; Conservative	6; Mismatches 7; Indels 0; Gaps 0;	

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 FT /note= "Complementarity determining region H1"
 FT 164..177
 FT /label= HFR2
 FT /note= "Heavy chain framework region 2"
 FT 178..194
 FT /label= CDR_H2
 FT /note= "Complementarity determining region H2"
 FT 195..226
 FT /label= HFR3
 FT /note= "Heavy chain framework region 3"
 FT 227..236
 FT /label= CDR_H3
 FT /note= "Complementarity determining region H3"
 FT 237..247
 FT /label= HFR4
 FT /note= "Heavy chain framework region 4"
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 PN WO2003040384-A1.
 XX
 XX 15-MAY-2003.
 XX
 XX 05-NOV-2002; 2002WO-US035567.
 XX
 XX 05-NOV-2001; 2001US-0332849P.
 XX
 XX (TEXA) UNIV TEXAS SYSTEM.
 XX
 XX Georgiou G, Iversen BL, Maynard JA;
 XX
 XX WPI; 2003-430672/40.
 XX
 XX New purified affinity-matured recombinant antibody with binding
 PT specificity for Bacillus anthracis protective antigen, useful for
 PT diagnosing, preventing or treating anthrax or other bacterial infections.
 PT
 XX Example; Page; 48pp; English.
 XX
 XX This invention relates a purified affinity-matured recombinant antibody
 CC or its portion having binding specificity for a proteinaceous toxin or a
 CC Bacillus anthracis protective antigen. The antibody may have an
 CC antibacterial activity and may be used in gene therapy or a vaccine.
 CC Bacillus anthracis, commonly referred to as was one of the first
 CC biological warfare agents to be developed and is now perceived as a major
 CC threat worldwide. The composition and methods of the invention may be
 CC useful in diagnosing, preventing or treating infections caused by
 CC Bacillus anthracis and other bacterial toxins. The present sequence is
 CC that of the mouse wild-type anti-protective antigen hybridoma antibody
 CC 14B7 scFv mutant A2E, with a synthetic linker (Gly4Ser)4 between the
 CC light and heavy chains. This antibody had a Ser55Pro substitution
 CC compared to the wild-type sequence (see AAO27252) and was developed in
 CC the examples of the specification in order to identify antibodies which
 CC had increased binding affinity for the Bacillus anthracis toxin. Note:
 CC This sequence does not appear in the specification but was created by the
 CC indexer using information given in the examples and figure 4 of the
 CC disclosure
 XX
 XX Sequence 247 AA;
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 XX Query Match 94.5%; Score 1243; DB 6; Length 247;
 XX Best Local Similarity 94.7%; Pred. No. 5.3e-77;
 XX Matches 234; Conservative 5; Mismatches 8; Indels 0; Gaps 0;
 QY 1 DIQMTTSSLSASLGDRVTVSCASQDIRNLNLYWYQKPDGTVKELIYTSRLLPVPS 60
 DB 1 DIQMTTSSLSASLGDRVTVSCASQDIRNLNLYWYQKPDGTVKELIYTSRLLPVPS 60
 QY 61 RFGSGSGTDYSLTNINLEQEDIGTYFCQGNTPPTPGGCTKLEIKRGGSGSGG 120
 DB 61 RFGSGSGTDYSLTNINLEQEDIGTYFCQGNTPPTPGGCTKLEIKRGGSGSGG 120
 QY 121 GSGGGGGSEVOLQSGPELVKPGASVKISKDSGYAFSSWVWVKRPGQGLEWIGRIY 180

DB 121 GSGGGGGSEVOLQSGPELVKPGASVKISKDSGYAFSSWVWVKRPGQGLEWIGRIY 180
 QY 181 PGDGDNYNGKTEGKAILTADKSSSTAYNQLSLSVDSAVYFCARSGLLRYAMDYWGQG 240
 DB 181 PGDGDNYNGKTEGKAILTADKSSSTAYNQLSLSVDSAVYFCARSGLLRYAMDYWGQG 240
 QY 241 TSVTVSS 247
 DB 241 TSVTVSS 247
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 ID AAO27255 standard; protein; 247 AA.
 XX
 AC AAO27255;
 XX
 DT 17-SEP-2003 (first entry)
 XX
 DE Antibody 14B7 scFv mutant 6A amino acid sequence.
 XX
 DE Mouse; murine; affinity-matured recombinant antibody;
 KW proteinaceous toxin; Bacillus anthracis protective antigen;
 KW antibacterial; gene therapy; vaccine; biological warfare agent;
 KW infection; hybridoma; scFv; 14B7; mutant; mutein; 6A.
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 OS Mus sp.
 OS Synthetic.
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 FT Region 1..23
 FT /label= LFR1
 FT /note= "Light chain framework region 1"
 FT 24..34
 FT /label= CDR_L1
 FT /note= "Complementarity determining region L1"
 FT 35..49
 FT /label= LFR2
 FT /note= "Light chain framework region 2"
 FT Misc-difference 46
 FT /note= "Wild-type Leu substituted by Phe"
 FT Region 50..56
 FT /label= CDR_L2
 FT /note= "Complementarity determining region L2"
 FT Misc-difference 56
 FT /note= "Wild-type Ser substituted by Pro"
 FT Region 57..88
 FT /label= LFR3
 FT /note= "Light chain framework region 3"
 FT Region 89..97
 FT /label= CDR_L3
 FT /note= "Complementarity determining region L3"
 FT 98..108
 FT /label= LFR4
 FT /note= "Light chain framework region 4"
 FT 109..128
 FT /label= Linker
 FT /note= "(Gly4Ser)4 linker"
 FT Misc-difference 118
 FT /note= "Wild-type Ser substituted by Thr"
 FT Region 129..247
 FT /label= Heavy_chain
 FT Region 129..154
 FT /label= HFR1
 FT /note= "Heavy chain framework region 1"
 FT 155..163
 FT /label= CDR_H1
 FT /note= "Complementarity determining region H1"
 FT 164..177
 FT /label= HFR2
 FT /note= "Heavy chain framework region 2"

FT Region 178..194
 FT /label= CDR_H2
 FT /note= "Complementarity determining region H2"
 FT 195..226
 FT /label= HFR3
 FT /note= "Heavy chain framework region 3"
 FT Misc-difference 207
 FT /note= "Wild-type Ala substituted by Glu"
 FT 227..236
 FT /label= CDR_H3
 FT /note= "Complementarity determining region H3"
 FT 237..247
 FT /label= HFR4
 FT /note= "Heavy chain framework region 4"
 FT
 PN WO2003040384-A1.
 XX
 XX 15-MAY-2003.
 XX
 XX 05-NOV-2002; 2002WO-US035567.
 XX
 XX 05-NOV-2001; 2001US-0332849P.
 XX
 XX (TEXA) UNIV TEXAS SYSTEM.
 PA
 PA Georgiou G, Iverson BL, Maynard JA;
 PI WPI; 2003-430672/40.
 DR
 XX New purified affinity-matured recombinant antibody with binding
 FT specificity for Bacillus anthracis protective antigen, useful for
 FT diagnosing, preventing or treating anthrax or other bacterial infections.
 FT
 XX Example; Page; 48pp; English.
 PS
 XX This invention relates a purified affinity-matured recombinant antibody
 CC or its portion having binding specificity for a proteinaceous toxin or a
 CC Bacillus anthracis protective antigen. The antibody may have an
 CC antibacterial activity and may be used in gene therapy or a vaccine.
 CC Bacillus anthracis, commonly referred to as was one of the first
 CC biological warfare agents to be developed and is now perceived as a major
 CC threat worldwide. The composition and methods of the invention may be
 CC useful in diagnosing, preventing or treating infections caused by
 CC Bacillus anthracis and other bacterial toxins. The present sequence is
 CC that of the mouse wild-type anti-protective antigen hybridoma antibody
 CC 14B7 scFv mutant 6A, with a synthetic linker (Gly4Ser)4 between the light
 CC and heavy chains. This antibody had Leu46Phe, Ser56Pro, Ser118Thr and
 CC Ala207Glu substitutions compared to the wild-type sequence (see AAO27252)
 CC and was developed in the examples of the specification in order to
 CC identify antibodies which had increased binding affinity for the Bacillus
 CC anthracis toxin. Note: This sequence does not appear in the specification
 CC but was created by the indexer using information given in the examples
 CC and figure 4 of the disclosure
 XX
 SQ Sequence 247 AA;
 Query Match 94.4%; Score 1242; DB 6; Length 247;
 Best Local Similarity 94.3%; Pred. No. 6.2e-77;
 Matches 233; Conservative 6; Mismatches 8; Indels 0; Gaps 0;
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 DB 1 DIQMTQTSSLSASLGRVTVSCRASQDIRNLYNWYQKPDGTVKFLIYTSRLPGVPS 60
 QY 61 RFGSGSGGTDSLTLNLEQEDIGTYFCQGNTPPTWFGGTTKLEIKRGGGSDGGSGG 120
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 QY 121 GSGGGGSEVQLQSQGPELVKPGASVKISCKDSGYAFNNSMMNWVQRPQGLIEWIGRIY 180
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DB 181 PGDGDNYNGKFKGKATLTADKSSSTAYMQLSSITSVDSAVYFCARSGLLRYAMDYWGQG 240
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 RESULT 4
 AAO27252
 ID AAO27252 standard; protein; 247 AA.
 XX
 AC AAO27252;
 XX
 DT 17-SEP-2003 (first entry)
 XX
 DE Antibody 14B7 scFv wild type amino acid sequence.
 XX
 KW Mouse, murine; affinity-matured recombinant antibody;
 KW proteinaceous toxin; Bacillus anthracis protective antigen;
 KW antibacterial; gene therapy; vaccine; biological warfare agent;
 KW infection; hybridoma; scFv; 14B7.
 XX
 OS Mus sp.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Region 1..108
 FT /label= Light_chain
 FT Region 1..23
 FT /label= LFR1
 FT /note= "Light chain framework region 1"
 FT Region 24..34
 FT /label= CDR_L1
 FT /note= "Complementarity determining region L1"
 FT Region 35..49
 FT /label= LFR2
 FT /note= "Light chain framework region 2"
 FT Region 50..56
 FT /label= CDR_L2
 FT /note= "Complementarity determining region L2"
 FT Region 57..88
 FT /label= LFR3
 FT /note= "Light chain framework region 3"
 FT Region 89..97
 FT /label= CDR_L3
 FT /note= "Complementarity determining region L3"
 FT Region 98..108
 FT /label= LFR4
 FT /note= "Light chain framework region 4"
 FT Region 109..128
 FT /label= Linker
 FT /note= "(Gly4Ser)4 linker"
 FT Region 129..247
 FT /label= Heavy_chain
 FT Region 129..154
 FT /label= HFR1
 FT /note= "Heavy chain framework region 1"
 FT Region 155..163
 FT /label= CDR_H1
 FT /note= "Complementarity determining region H1"
 FT Region 164..177
 FT /label= HFR2
 FT /note= "Heavy chain framework region 2"
 FT Region 178..194
 FT /label= CDR_H2
 FT /note= "Complementarity determining region H2"
 FT Region 195..226
 FT /label= HFR3
 FT /note= "Heavy chain framework region 3"
 FT Region 227..236
 FT /label= CDR_H3
 FT /note= "Complementarity determining region H3"

FT Region 237..247
FT /label= HFR4
FT /note= "Heavy chain framework region 4"
FN WO2003040384-A1.
XX 15-MAY-2003.
XX 05-NOV-2002; 2002WO-US035567.
XX 05-NOV-2001; 2001US-0332849P.
XX (TEXA) UNIV TEXAS SYSTEM.
XX Georgiou G, Iverson BL, Maynard JA;
XX WPI; 2003-430672/40.
XX New purified affinity-matured recombinant antibody with binding
FT specificity for Bacillus anthracis protective antigen, useful for
FT diagnosing, preventing or treating anthrax or other bacterial infections.
XX Example; Fig 4; 48pp; English.
PS CC This invention relates a purified affinity-matured recombinant antibody
CC or its portion having binding specificity for a proteinaceous toxin or a
CC Bacillus anthracis protective antigen. The antibody may have an
CC antibacterial activity and may be used in gene therapy or a vaccine.
CC Bacillus anthracis, commonly referred to as was one of the first
CC biological warfare agents to be developed and is now perceived as a major
CC threat worldwide. The composition and methods of the invention may be
CC useful in diagnosing, preventing or treating infections caused by
CC Bacillus anthracis and other bacterial toxins. The present sequence is
CC that of the mouse wild-type anti-protective antigen hybridoma antibody
CC 14B7 scFv, with a synthetic linker (Gly4Ser)4 between the light and heavy
CC chains. This antibody was used for the development of mutant antibodies
CC (see AAO27253-6) which had increased binding affinity for the Bacillus
CC anthracis toxin in the examples of the specification
XX
SQ Sequence 247 AA;
Query Match 93.8%; Score 1235; DB 6; Length 247;
Best Local Similarity 94.3%; Pred. No. 1.9e-76;
Matches 233; Conservative 5; Mismatches 9; Indels 0; Gaps 0;
QY 1 DIQMOTSSLSASLGDRVTVCASQDIRNLNWKQKPDGTVKFLIYYTSRLPGVPS 60
Db 1 DIQMOTSSLSASLGDRVTVCASQDIRNLNWKQKPDGTVKFLIYYTSRLQSGVPS 60
QY 61 RPSGGSGTDYSLTINNLEQEDIGTYFCQGNTPWTGGTGLKIKRGGSGSGGSGG 120
Db 61 RPSGGSGTDYSLTISNQEDIGTYFCQGNTPWTGGTGLKIKRGGSGSGGSGG 120
QY 121 GSGGGSGEVQLQDSPELVKPGASVKLSCKDSGYAFNWSMNWKQRPQGLEWIGRIY 180
Db 121 GSGGGSGEVQLQDSPELVKPGASVKLSCKDSGYAFNWSMNWKQRPQGLEWIGRIY 180
QY 181 PGDGSNNGKPEGKAILTADKSSSTAYNQLSSLTVDVSAVYFCARSGLLRYAMDWQG 240
Db 181 PGDGTNYNGKKGKATLTADKSSSTAYNQLSSLTVDVSAVYFCARSGLLRYAMDWQG 240
QY 241 TSVTVSS 247
Db 241 TSVTVSS 247
RESULT 5
AAO27256
ID AAO27256 standard; protein; 247 AA.
XX
AC AAO27256;
XX
DT 17-SEP-2003 (first entry)

XX Antibody 14B7 scFv mutant L97 amino acid sequence.
XX Mouse; murine; affinity-matured recombinant antibody;
KW proteinaceous toxin; Bacillus anthracis protective antigen;
KW antibacterial; gene therapy; vaccine; biological warfare agent;
XX infection; hybridoma; scFv; 14B7; mutant; mutein; L97.
XX Mus sp.
OS Synthetic.
XX Key
XX Location/Qualifiers
FT 1..108
FT /label= Light_chain
FT 1..23
FT /label= LFR1
FT /note= "Light chain framework region 1"
FT 24..34
FT /label= CDR_L1
FT /note= "Complementarity determining region L1"
FT 35..49
FT /label= LFR2
FT /note= "Light chain framework region 2"
FT 50..56
FT /label= CDR_L2
FT /note= "Complementarity determining region L2"
FT 57..88
FT /label= LFR3
FT /note= "Light chain framework region 3"
FT 89..97
FT /label= CDR_L3
FT /note= "Complementarity determining region L3"
FT 98..108
FT /label= LFR4
FT /note= "Light chain framework region 4"
FT 109..128
FT /label= Linker
FT /note= "(Gly4Ser) 4 linker"
FT 129..247
FT /label= Heavy_chain
FT 129..154
FT /label= HFR1
FT /note= "Heavy chain framework region 1"
FT 155..163
FT /label= CDR_H1
FT /note= "Complementarity determining region H1"
FT 164..177
FT /label= HFR2
FT /note= "Heavy chain framework region 2"
FT 178..194
FT /label= CDR_H2
FT /note= "Complementarity determining region H2"
FT 195..226
FT /label= HFR3
FT /note= "Heavy chain framework region 3"
FT 227..236
FT /label= CDR_H3
FT /note= "Complementarity determining region H3"
FT Misc-difference 229
FT /note= "Wild-type Leu substituted by Ala"
FT 237..247
FT /label= HFR4
FT /note= "Heavy chain framework region 4"
XX WO2003040384-A1.
XX 15-MAY-2003.
XX 05-NOV-2002; 2002WO-US035567.
XX 05-NOV-2001; 2001US-0332849P.
XX (TEXA) UNIV TEXAS SYSTEM.

Db 508 GSGGGGSEVQLQSGPELVKPGASMKISKASGYSFTGTMNWKSHQKLNEMWGLIN 567
 Qy 181 PGDGSNYNGFEGKAILTADKSSSTAYMQLSSLTSDSAVYFCARSGLL---RYAMDYV 237
 Db 568 PYKGVSTYNQKFKDKAFTVDKSSSTAYMQLSSLTSDSAVYFCARSGLLSDWYFDYV 627
 Qy 238 GQGTSTVTSS 247
 Db 628 GQGTSTVTSS 637

RESULT 7
 AAU75370
 ID AAU75370 standard; protein; 638 AA.
 XX AC AAU75370;
 XX DT 23-APR-2002 (first entry)
 XX DE Diphtheria toxin/UCHT1 immunotoxin fusion protein #6.
 XX KW Immunotoxin; pseudomonas exotoxin A; ETA; diphtheria toxin; DT;
 KW cystostatic; immunosuppressive; immunostimulant; antidiabetic;
 KW antirheumatic; antiarthritic; anti-HIV; anti-inflammatory;
 KW anti-T cell immunotoxin fusion protein; antibody; UCHT1;
 KW (Gly4Ser)3 linker; T cell leukaemia; lymphoma; graft-versus-host disease;
 KW Fv; autoimmune disease; transplant rejection;
 KW systemic lupus erythematosus; type I diabetes; rheumatoid arthritis;
 KW myasthenia gravis; multiple sclerosis; AIDS;
 KW acquired immunodeficiency syndrome; chronic immunosuppression.
 XX Mus sp.
 OS Corynebacterium diphtheriae.
 OS Synthetic.
 OS Chimeric.
 XX W0200187982-A2.
 XX 22-NOV-2001.
 XX PF 18-MAY-2001; 2001WO-US016125.
 XX PR 18-MAY-2000; 2000US-00573797.
 XX PA (NOVS) NOVARTIS AG.
 XX PA (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.
 XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX PI Neville DM, Thompson JT, Hu H, Woo J, Ma S, Hexham JM, Digan ME;
 XX WPI; 2002-121980/16.
 XX New anti-T cell immunotoxin fusion protein comprising a truncated
 PT diphtheria toxin moiety, a connector, and one single chain Fv of the
 PT variable region of a UCHT1 antibody, useful for treating e.g. autoimmune
 PT diseases.
 XX Claim 19; Page 269-270; 307pp; English.
 XX The invention relates to an anti-T cell immunotoxin fusion protein,
 CC comprising from the amino terminus, a truncated diphtheria toxin moiety,
 CC a connector, and one single chain Fv of the variable region of a UCHT1
 CC antibody. The single chain Fv comprises VL, L, or VH, L is a Gly-Ser
 CC linker, and VL and VH are the variable light and heavy domains of the
 CC anti-CD3 antibody UCHT1. Also included are a nucleic acid encoding the
 CC novel immunotoxin fusion protein, a vector comprising the nucleic acid
 CC and a cell comprising the nucleic acid. The immunotoxin may also be a
 CC pseudomonas endotoxin A (ETA). The immunotoxins are useful for treating T
 CC cell leukaemias or lymphomas, graft-versus-host diseases, and autoimmune
 CC diseases by inducing immune tolerance. The immunotoxin fusion proteins
 CC may be used in vivo to systemically reduce populations of T cells, or ex
 CC vivo to effect T-cell depletion from a treated cell population. The
 CC fusion proteins can be administered to a subject who is or will be a

CC recipient of an allotransplant to prevent or reduce T-cell mediated acute
 CC or chronic transplant rejection of the transplanted allogeneic cells,
 CC tissue or organ in the subject as well as treat other T-cell mediated
 CC diseases such as systemic lupus erythematosus, type I diabetes,
 CC rheumatoid arthritis, myasthenia gravis, multiple sclerosis, infectious
 CC diseases of the immune system (e.g. AIDS (acquired immunodeficiency
 CC syndrome)) and chronic immunosuppression. The present sequence is an
 CC immunotoxin fusion protein of the invention comprising 330 residues from
 CC the N-terminal glycine of mature DT toxin, a (Gly4Ser)3 linker and one
 CC single Fv chain from antibody UCHT1
 XX
 XX Sequence 638 AA;
 Query Match 75.3%; Score 991; DB 5; Length 638;
 Best Local Similarity 78.0%; Pred. No. 1.9e-59;
 Matches 195; Conservative 13; Mismatches 34; Indels 8; Gaps 2;
 QY 1 DIQMTQTSSLSASLGDRVTVCSCASQDIRNYLNWYQKPDGTVKFLIYYTSRLPGVPS 60
 Db 394 DIQMTQTSSLSASLGDRVTVCSCASQDIRNYLNWYQKPDGTVKFLIYYTSRLHSGVPS 453
 QY 61 RESGSGSGDYSLTINNLEQEDIGTYFCQOQNTPTTGGTKLEIKSGGGSDGGSGG 120
 Db 454 KFSGSGSGDYSLTINNLEQEDIGTYFCQOQNTPTTGGTKLEIKSGGGSDGGSGG 508
 QY 121 GSGSGGGSEVQLQSGPELVKPGASVKISKDSGSAFNSWMNWKQRPQGLEWIGRIY 180
 Db 509 GSGSGGGSEVQLQSGPELVKPGASVKISKDSGSAFNSWMNWKQRPQGLEWIGRIY 568
 QY 181 PGDGSNYNGFEGKAILTADKSSSTAYMQLSSLTSDSAVYFCARSGLL---RYAMDYV 237
 Db 569 PYKGVSTYNQKFKDKAFTVDKSSSTAYMQLSSLTSDSAVYFCARSGLLSDWYFDYV 628
 QY 238 GQGTSTVTSS 247
 Db 629 GQGTSTVTSS 638

RESULT 8
 AAU75383
 ID AAU75383 standard; protein; 656 AA.
 XX AC AAU75383;
 XX DT 23-APR-2002 (first entry)
 XX DE Immunotoxin fusion protein related sequence #2.
 XX KW Immunotoxin; pseudomonas exotoxin A; ETA; diphtheria toxin; DT;
 KW cystostatic; immunosuppressive; immunostimulant; antidiabetic;
 KW antirheumatic; antiarthritic; anti-HIV; anti-inflammatory;
 KW anti-T cell immunotoxin fusion protein; antibody; scUCHT1; Fv; CD3;
 KW T cell leukaemia; lymphoma; graft-versus-host disease;
 KW autoimmune disease; transplant rejection; systemic lupus erythematosus;
 KW type I diabetes; rheumatoid arthritis; myasthenia gravis;
 KW multiple sclerosis; AIDS; acquired immunodeficiency syndrome;
 KW chronic immunosuppression.
 XX Unidentified.
 XX W0200187982-A2.
 XX 22-NOV-2001.
 XX PF 18-MAY-2001; 2001WO-US016125.
 XX PR 18-MAY-2000; 2000US-00573797.
 XX PA (NOVS) NOVARTIS AG.
 XX PA (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.
 XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX PI Neville DM, Thompson JT, Hu H, Woo J, Ma S, Hexham JM, Digan ME;

XX WPI; 2002-121980/16.
 XX New anti-T cell immunotoxin fusion protein comprising a truncated
 PT diphtheria toxin moiety, a connector, and one single chain Fv of the
 PT variable region of a UCHL1 antibody, useful for treating e.g. autoimmune
 PS diseases.
 PS Disclosure; Page 282-283; 307pp; English.
 XX
 XX The invention relates to an anti-T cell immunotoxin fusion protein,
 CC comprising from the amino terminus, a truncated diphtheria toxin moiety,
 CC a connector, and one single chain Fv of the variable region of a UCHL1
 CC antibody. The single chain Fv comprises VL, L, or VH, L is a Gly-Ser
 CC linker, and VL and VH are the variable light and heavy domains of the
 CC anti-CD3 antibody UCHL1. Also included are a nucleic acid encoding the
 CC novel immunotoxin fusion protein, a vector comprising the nucleic acid
 CC and a cell comprising the nucleic acid. The immunotoxin may also be a
 CC pseudomonas endotoxin A (ETA). The immunotoxins are useful for treating T
 CC cell leukemias or lymphomas, graft-versus-host diseases, and autoimmune
 CC diseases by inducing immune tolerance. The immunotoxin fusion proteins
 CC may be used in vivo to systemically reduce populations of T cells, or ex
 CC vivo to effect T-cell depletion from a treated cell population. The
 CC fusion proteins can be administered to a subject who is or will be a
 CC recipient of an allotransplant to prevent or reduce T-cell mediated acute
 CC or chronic transplant rejection of the transplanted allogeneic cells,
 CC tissue or organ in the subject as well as treat other T-cell mediated
 CC diseases such as systemic lupus erythematosus, type I diabetes,
 CC rheumatoid arthritis, myasthenia gravis, multiple sclerosis, infectious
 CC diseases of the immune system (e.g. AIDS (acquired immunodeficiency
 CC syndrome)) and chronic immunosuppression. The present sequence is a
 CC protein sequence included in the sequence listing but not mentioned
 CC elsewhere in the specification, associated with the immunotoxin fusion
 CC proteins of the invention
 XX
 XX Sequence 656 AA;
 SQ
 Query Match 75.3%; Score 991; DB 5; Length 656;
 Best Local Similarity 78.0%; Pred. No. 1.9e-59;
 Matches 195; Conservative 13; Mismatches 34; Indels 8; Gaps 2;
 QY 1 DIQMTQTSSLSASLGDRVTVCSCASQDIENLYNWQKPDGTVKFLIYTSRLLPVPS 60
 DB 412 DIQMTQTSSLSASLGDRVTVCSCASQDIENLYNWQKPDGTVKFLIYTSRLHSGVPS 471
 QY 61 RFGSGSGTDYSLTINNLEQEDIGYFCQQGNTPEWTFGGGTKLEIKRGGSGSGG 120
 DB 472 RFGSGSGTDYSLTINNLEQEDIGYFCQQGNTPEWTFGGGTKLEIKRGGSGG 526
 QY 121 GSGGGGSEVQLQSGPELVKPGASVKISKDSGYAFNNSWNNWYKQPGGLEWIGRIY 180
 DB 527 GSGGGGSEVQLQSGPELVKPGASVKISKDSGYAFNNSWNNWYKQPGGLEWIGRIY 586
 QY 181 PGDGSNNYKPEGRKAILTADKSSSTAYNQLSSLTSDSVAVFYCARSGLL---RYAMDY 237
 DB 587 PKGVSTYKQPKDATTVDKSSSTAYNQLSSLTSDSVAVFYCARSGYGDSDWYPDVW 646
 QY 238 GQGTSTVTS 247
 DB 647 GQGTTLTVFS 656
 RESULT 9
 AAU75389
 ID AAU75389 standard; protein; 657 AA.
 XX
 XX AAU75389;
 XX
 XX 23-APR-2002 (first entry)
 XX Diphtheria toxin/UCHL1 immunotoxin fusion protein HisDT390-sFv.
 XX Immunotoxin; pseudomonas exotoxin A; ETA; diphtheria toxin; DT;

KW cytostatic; immunosuppressive; immunostimulant; antidiabetic;
 KW antirheumatic; antiarthritis; anti-HIV; anti-inflammatory;
 KW anti-T cell immunotoxin fusion protein; antibody; UCHL1;
 KW (Gly4Ser)3 linker; T cell leukaemia; lymphoma; graft-versus-host disease;
 KW Fv; autoimmune disease; transplant rejection;
 KW systemic lupus erythematosus; type I diabetes; rheumatoid arthritis;
 KW myasthenia gravis; multiple sclerosis; AIDS; HisDT390-sFv;
 KW acquired immunodeficiency syndrome; chronic immunosuppression.
 XX
 XX Mus sp.
 OS Corynebacterium diphtheriae.
 OS Synthetic.
 OS Chimeric.
 XX
 PN W0200187982-A2.
 XX
 XX 22-NOV-2001.
 PD
 PF 18-MAY-2001; 2001WO-US016125.
 PF
 XX 18-MAY-2000; 2000US-00573797.
 XX
 XX (NOVS) NOVARTIS AG.
 FA (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 PI Neville DM, Thompson JT, Hu H, Woo J, Ma S, Hexham JM, Digan ME;
 XX WPI; 2002-121980/16.
 XX
 XX New anti-T cell immunotoxin fusion protein comprising a truncated
 PT diphtheria toxin moiety, a connector, and one single chain Fv of the
 PT variable region of a UCHL1 antibody, useful for treating e.g. autoimmune
 PT diseases.
 XX
 XX Example 30; Fig 34; 307pp; English.
 XX
 CC The invention relates to an anti-T cell immunotoxin fusion protein,
 CC comprising from the amino terminus, a truncated diphtheria toxin moiety,
 CC a connector, and one single chain Fv of the variable region of a UCHL1
 CC antibody. The single chain Fv comprises VL, L, or VH, L is a Gly-Ser
 CC linker, and VL and VH are the variable light and heavy domains of the
 CC anti-CD3 antibody UCHL1. Also included are a nucleic acid encoding the
 CC novel immunotoxin fusion protein, a vector comprising the nucleic acid
 CC and a cell comprising the nucleic acid. The immunotoxin may also be a
 CC pseudomonas endotoxin A (ETA). The immunotoxins are useful for treating T
 CC cell leukemias or lymphomas, graft-versus-host diseases, and autoimmune
 CC diseases by inducing immune tolerance. The immunotoxin fusion proteins
 CC may be used in vivo to systemically reduce populations of T cells, or ex
 CC vivo to effect T-cell depletion from a treated cell population. The
 CC fusion proteins can be administered to a subject who is or will be a
 CC recipient of an allotransplant to prevent or reduce T-cell mediated acute
 CC or chronic transplant rejection of the transplanted allogeneic cells,
 CC tissue or organ in the subject as well as treat other T-cell mediated
 CC diseases such as systemic lupus erythematosus, type I diabetes,
 CC rheumatoid arthritis, myasthenia gravis, multiple sclerosis, infectious
 CC diseases of the immune system (e.g. AIDS (acquired immunodeficiency
 CC syndrome)) and chronic immunosuppression. The present sequence is an
 CC immunotoxin fusion protein of the invention comprising 390 residues from
 CC the N-terminal glycine of mature DT toxin, a linker and one single Fv
 CC chain from antibody UCHL1, HisDT390-sFv
 XX
 XX Sequence 657 AA;
 SQ
 Query Match 75.3%; Score 991; DB 5; Length 657;
 Best Local Similarity 78.0%; Pred. No. 1.9e-59;
 Matches 195; Conservative 13; Mismatches 34; Indels 8; Gaps 2;
 QY 1 DIQMTQTSSLSASLGDRVTVCSCASQDIENLYNWQKPDGTVKFLIYTSRLLPVPS 60
 DB 413 DIQMTQTSSLSASLGDRVTVCSCASQDIENLYNWQKPDGTVKFLIYTSRLHSGVPS 472
 QY 61 RFGSGSGTDYSLTINNLEQEDIGYFCQQGNTPEWTFGGGTKLEIKRGGSGSGG 120

Db 473 KFGSGSGTGYSLTINLEQEDTATYFCQGNLTLPWTFFAGTKLEIKRG-----GGSGG 527
Qy 121 GSGSGGSEVQLQSGPELVKPGASVKISCKDGYAFNNSMMWVVKQRPQGGLEWIGRIY 180
Db 528 GSGSGGSEVQLQSGPELVKPGASVKISCKASGYSGFTGMWVKQSHGKNLEWMLIN 587
Qy 181 PGDGSNNGKPEGKAILTADKSSSTAYMQLSSLTSDSAVYFCARSGLL---RYAMDYW 237
Db 588 FYKGVSTYNQKPKDKATFTVDKSSSTAYMQLSSLTSDSAVYFCARSGLL---RYAMDYW 237
Qy 238 GQGTSTVTSS 247
Db 648 GQGTSTVTSS 657

RESULT 10
AAB07461
ID AAB07461 standard; protein; 601 AA.
XX AAB07461;
XX 20-OCT-2000 (first entry)
XX An immunotoxin comprising a CD3 binding domain and PE28.
XX Immunotoxin; CD3-binding domain; Pseudomonas exotoxin A; immune system;
XX scFv(UCHT-1)-PE28; T-cell mediated disease; transplant rejection;
XX host versus graft disease; graft versus host disease;
XX bone marrow transplant.
XX Synthetic.
XX Mus sp.
XX Pseudomonas aeruginosa.
XX Key Location/Qualifiers
XX Region 3..112
XX /note= "variable region of the light chain"
XX Region 128..249
XX /note= "variable region of the heavy chain"
XX WO200041474-A2.
XX
XX 20-JUL-2000.
XX
XX 13-JAN-2000; 2000WO-BF000245.
XX
XX 15-JAN-1999; 99US-00232445.
XX 25-JAN-1999; 99US-00236968.
XX 07-OCT-1999; 99US-00414134.
XX
XX (NOVS) NOVARTIS AG.
XX (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.
XX
XX Digan ME, Lake P, Wright RM;
XX
XX WPI; 2000-482739/42.
XX N-PSDB; AAA58773.
XX
XX Recombinant immunotoxin used for prophylaxis and treatment of T-cell
XX mediated diseases e.g. transplantation rejection.
XX
XX Claim 3; Page 60-63; 75pp; English.
XX
XX The present sequence represents a recombinant immunotoxin comprising a
XX CD3-binding domain and a Pseudomonas exotoxin A component. It is
XX designated scFv(UCHT-1)-PE28. The immunotoxins of the invention are used
XX for the prophylaxis or treatment of T-cell mediated diseases or
XX conditions of the immune system. They are also used to condition a
XX patient to be transplanted with cells, or a tissue or an organ of a donor
XX and for the prophylaxis and/or treatment of acute or chronic
XX transplantation rejection, host versus graft disease and/or graft versus
XX host disease in a patient to undergo a bone marrow transplant, where the

CC CD3-bearing cell population in the patient is depleted and an inoculum
CC comprising isolated bone marrow and/or stem-cell enriched peripheral
CC blood cells of the donor treated with immunotoxin is inoculated into the
CC patient
XX
SQ Sequence 601 AA;
Query Match 75.2%; Score 989; DB 3; Length 601;
Best Local Similarity 78.8%; Pred. No. 2.4e-59;
Matches 197; Conservative 12; Mismatches 35; Indels 6; Gaps 3;
Qy 1 DIQMTQTTSLSASLGDRVTISCRASQDIRNYLNWYQKPDGTVKFLIYTSRLPGVPS 60
Db 3 DIQMTQTTSLSASLGDRVTISCRASQDIRNYLNWYQKPDGTVKFLIYTSRLPGVPS 62
Qy 61 RESGSGSGTDYSLTINLEQEDIGTYFCQGNLTLPWTFFAGTKLEIKRGSGSG 120
Db 63 KFGSGSGTDYSLTINLEQEDIGTYFCQGNLTLPWTFFAGTKLEIKRGSGSG 121
Qy 121 GSGSGGSEVQLQSGPELVKPGASVKISCKDGYAFNNSMMWVVKQRPQGGLEWIGRIY 180
Db 122 G--SGSGSEVQLQSGPELVKPGASVKISCKASGYSGFTGMWVKQSHGKNLEWMLIN 179
Qy 181 PGDGSNNGKPEGKAILTADKSSSTAYMQLSSLTSDSAVYFCARSGLL---RYAMDYW 237
Db 180 FYKGVSTYNQKPKDKATFTVDKSSSTAYMQLSSLTSDSAVYFCARSGLL---RYAMDYW 239
Qy 238 GQGTSTVTSS 247
Db 240 GAGTTVTSS 249

RESULT 11
AABG72265
ID AABG72265 standard; protein; 601 AA.
XX AABG72265;
XX 06-MAR-2003 (first entry)
XX Recombinant immunotoxin, scFv(UCHT-1)-PE38.
XX Recombinant immunotoxin; scFv(UCHT-1)-PE38; single chain Fv fragment;
XX murine; anti-human CD3-monoclonal antibody binding domain; UCHT-1;
XX Pseudomonas aeruginosa; exotoxin A; ADP-ribosylating; translocation;
XX T-cell mediated disorder; organ transplantation rejection;
XX autoimmune disease; graft versus host disease; bone marrow transplant;
XX acquired immunodeficiency syndrome; AIDS; T-cell leukaemia;
XX T-cell lymphoma; T-cell-mediated autoimmune disease; type I diabetes;
XX systemic lupus erythematosus; rheumatoid arthritis; myasthenia gravis;
XX multiple sclerosis; immunological tolerance; osteoporosis;
XX aplastic anaemia; Gaucher's disease; thalassaemia; mutant; mutein.
XX Mus sp.
XX Pseudomonas aeruginosa.
XX Synthetic.
XX Chimeric.
XX Key Location/Qualifiers
XX Region 3..111
XX /note= "Light chain variable region (VL)"
XX Peptide 112..127
XX /note= "Linker peptide (L)"
XX Region 128..249
XX /note= "Heavy chain variable region (VH)"
XX Peptide 250..254
XX /note= "Connector peptide (C)"
XX Region 255..601
XX /note= "PE38 mutant"
XX US2002142000-A1.
XX 03-OCT-2002.

PI Neville DM, Thompson JT, Hu H, Woo J, Ma S, Hexham JM, Digan ME;
 XX WPI; 2002-121980/16.
 XX
 XX New anti-T cell immunotoxin fusion protein comprising a truncated
 PT diphtheria toxin moiety, a connector, and one single chain Fv of the
 PT variable region of a UCHT1 antibody, useful for treating e.g. autoimmune
 PT diseases.
 XX
 XX Claim 7; Fig 34; 307pp; English.
 XX
 XX The invention relates to an anti-T cell immunotoxin fusion protein,
 CC comprising from the amino terminus, a truncated diphtheria toxin moiety,
 CC a connector, and one single chain Fv of the variable region of a UCHT1
 CC antibody. The single chain Fv comprises VL, L, or VH, L is a Gly-Ser
 CC linker, and VL and VH are the variable light and heavy domains of the
 CC anti-CD3 antibody UCHT1. Also included are a nucleic acid encoding the
 CC novel immunotoxin fusion protein, a vector comprising the nucleic acid
 CC and a cell comprising the nucleic acid. The immunotoxin may also be a
 CC pseudomonas endotoxin A (ETA). The immunotoxins are useful for treating T
 CC cell leukemias or lymphomas, graft-versus-host diseases, and autoimmune
 CC diseases by inducing immune tolerance. The immunotoxin fusion proteins
 CC may be used in vivo to systemically reduce populations of T cells, or ex
 CC vivo to effect T-cell depletion from a treated cell population. The
 CC fusion proteins can be administered to a subject who is or will be a
 CC recipient of an allotransplant to prevent or reduce T-cell mediated acute
 CC or chronic transplant rejection of the transplanted allogeneic cells,
 CC tissue or organ in the subject as well as treat other T-cell mediated
 CC diseases such as systemic lupus erythematosus, type I diabetes,
 CC rheumatoid arthritis, myasthenia gravis, multiple sclerosis, infectious
 CC diseases of the immune system (e.g. AIDS (acquired immunodeficiency
 CC syndrome)) and chronic immunosuppression. The present sequence is an
 CC immunotoxin fusion protein of the invention comprising 389 residues from
 CC the N-terminal glycine of mature DT toxin, a (Gly4Ser)3 linker and one
 CC single Fv chain from antibody UCHT1, DT389.scFv (UCHT1)
 XX
 XX Sequence 643 AA;
 SQ
 Query Match 75.2%; Score 989; DB 5; Length 643;
 Best Local Similarity 78.8%; Pred. No. 2.6e-59;
 Matches 197; Conservative 12; Mismatches 35; Indels 6; Gaps 3;
 QY 1 DIQMTQTSSLSASLGRVTVSCRASQDIRNLNWTQKPDGTGTVKFLIYVTSRLPGVPS 60
 DB 397 DIQMTQTSSLSASLGRVTVSCRASQDIRNLNWTQKPDGTGTVKFLIYVTSRLHSGVPS 456
 QY 61 RPSGSGSGTDYSLTINLNLEQEDIGTYFCQCGNTPTPTFGGKLEIKRGGSGDGGSGG 120
 DB 457 KPSGSGSGTDYSLTINLNLEQEDIGTYFCQCGNTPTPTFGGKLEIKRAGGSGG 515
 QY 121 GSGSGSGSEVLOQSGPELVKPGASVKISCKDSGYAFNSWMNVKQRPQGLEWIGRIY 180
 DB 516 G--SGGSGSEVLOQSGPELVKPGASVKISCKASGYSTGYTMMVKQSHKLNWGLIN 573
 QY 181 PGDGSNNGKFEKGKAILTADKSSSTAYMQLSLTSVDSAVYFCARSGLL---RYAMDYV 237
 DB 574 PYKGVSTYNQKFDKATLTVDKSSSTAYMQLSLTSVDSAVYFCARSGYTGSDWYFDVW 633
 QY 238 GQGTSTVTSS 247
 DB 634 GAGTTVTSS 643
 RESULT 15
 ID AAO29670 standard; protein; 643 AA.
 XX
 XX AAO29670;
 AC
 XX 22-SEP-2003 (first entry)
 DT
 XX
 XX Anti-T cell immunotoxin fusion protein #1.
 DE
 XX

KW Immunotoxin; anti-T cell; fusion protein; chemotherapeutic agent;
 KW diphtheria toxin; pseudomonas toxin; proliferative disease;
 KW T-cell leukemia; T-cell lymphoma; T-cell granular lymphatic leukaemia;
 KW aggressive natural killer cell leukaemia; hairy-cell leukaemia;
 KW Sezary syndrome; angioimmunoblastic T-cell lymphoma;
 KW cutaneous T-cell lymphoma.
 XX
 XX Unidentified.
 XX
 XX WO2003045429-A2.
 XX
 XX 05-JUN-2003.
 XX
 XX 27-NOV-2002; 2002WO-EP013387.
 XX
 XX 28-NOV-2001; 2001GB-00028510.
 XX
 XX (NOVS) NOVARTIS AG.
 XX (NOVS) NOVARTIS PHARMA GMBH.
 XX
 XX Engel G;
 XX
 XX WPI; 2003-482489/45.
 XX
 XX Combination for treating malignant proliferative disease, e.g. leukemia
 PT and lymphoma, has an anti-T cell immunotoxin fusion protein comprising a
 PT diphtheria/pseudomonas toxin and a targeting moiety, and a
 PT chemotherapeutic agent.
 XX
 XX Claim 7; Page 23-27; 66pp; English.
 XX
 XX The invention relates to a novel combination comprising an anti-T cell
 CC immunotoxin fusion protein and at least one chemotherapeutic agent. The
 CC fusion protein comprises a diphtheria or pseudomonas toxin moiety and a
 CC targeting moiety suitable for targeting the fusion protein to T cells.
 CC The novel combination is useful for preparing pharmaceutical composition
 CC that is useful for delaying the progression of or for the treatment of a
 CC malignant proliferative disease such as lymphoma or leukemia in a
 CC subject, in particular T-cell leukemia, T-cell lymphoma, including T-
 CC cell granular lymphatic leukaemia, aggressive natural killer cell
 CC leukemia, hairy-cell leukaemia, Sezary syndrome, angioimmunoblastic T-
 CC cell lymphoma, peripheral T-cell lymphoma unspecified, cutaneous T-cell
 CC lymphoma, subcutaneous panniculitis like T-cell lymphoma, and
 CC hepatocellular carcinoma/delta T-cell lymphoma. The present sequence is an
 CC example of anti-T cell immunotoxin fusion protein of the invention
 XX
 XX Sequence 643 AA;
 SQ
 Query Match 75.2%; Score 989; DB 6; Length 643;
 Best Local Similarity 78.8%; Pred. No. 2.6e-59;
 Matches 197; Conservative 12; Mismatches 35; Indels 6; Gaps 3;
 QY 1 DIQMTQTSSLSASLGRVTVSCRASQDIRNLNWTQKPDGTGTVKFLIYVTSRLPGVPS 60
 DB 397 DIQMTQTSSLSASLGRVTVSCRASQDIRNLNWTQKPDGTGTVKFLIYVTSRLHSGVPS 456
 QY 61 RPSGSGSGTDYSLTINLNLEQEDIGTYFCQCGNTPTPTFGGKLEIKRGGSGDGGSGG 120
 DB 457 KPSGSGSGTDYSLTINLNLEQEDIGTYFCQCGNTPTPTFGGKLEIKRAGGSGG 515
 QY 121 GSGSGSGSEVLOQSGPELVKPGASVKISCKDSGYAFNSWMNVKQRPQGLEWIGRIY 180
 DB 516 G--SGGSGSEVLOQSGPELVKPGASVKISCKASGYSTGYTMMVKQSHKLNWGLIN 573
 QY 181 PGDGSNNGKFEKGKAILTADKSSSTAYMQLSLTSVDSAVYFCARSGLL---RYAMDYV 237
 DB 574 PYKGVSTYNQKFDKATLTVDKSSSTAYMQLSLTSVDSAVYFCARSGYTGSDWYFDVW 633
 QY 238 GQGTSTVTSS 247
 DB 634 GAGTTVTSS 643

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Job time : 52 secs